

SEQUENCE LISTING

<110> Rock, Charles O
Heath, Richard J

<120> Novel Enoyl Reductases and Methods of Use Thereof

<130> SJ-0022

<140> US 09/498,520

<141> 2000-02-04

<160> 62

<170> PatentIn version 3.1

<210> 1

<211> 975

<212> DNA

<213> Streptococcus pneumoniae

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<210> 2

<211> 324

<212> PRT

<213> Streptococcus pneumoniae

<400> 2

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Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ser Leu Thr Asp Lys
50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Val Glu Asp Ile
65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
85 90 95

Gly Asn Pro Ser Lys Tyr Met Glu Arg Phe His Glu Ala Gly Ile Ile
100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys
115 120 125

Ile Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Ala Thr Ala
145 150 155 160

Ile Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly Glu Gly
165 170 175

Ala Ala Ala Gly Phe Met Leu Gly Ala Glu Ala Val Gln Val Gly Thr
180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Pro Asn Tyr Lys Glu
195 200 205

Lys Ile Leu Lys Ala Arg Asp Ile Asp Thr Thr Ile Ser Ala Gln His
210 215 220

Phe Gly His Ala Val Arg Ala Ile Lys Asn Gln Leu Thr Arg Asp Phe
225 230 235 240

Glu Leu Ala Glu Lys Asp Ala Phe Lys Glu Asp Pro Asp Leu Glu
245 250 255

Ile Phe Glu Gln Met Gly Ala Gly Ala Leu Ala Lys Ala Val Val His
260 265 270

Gly Asp Val Asp Gly Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu
275 280 285

Val Ser Lys Glu Glu Thr Ala Glu Glu Ile Leu Lys Asp Leu Tyr Tyr
290 295 300

Gly Ala Ala Lys Lys Ile Gln Glu Glu Ala Ser Arg Trp Thr Gly Val
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Val Arg Asn Asp

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<212> DNA
<213> Streptococcus mutans

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 <212> PRT
 <213> Streptococcus mutans

<400> 4

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 20 25 30

Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
 35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ala Val Thr Asn Lys
 50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile
 65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
 85 90 95

Gly Asn Pro Gly Lys Tyr Ile Glu Arg Phe His Glu Ala Gly Ile Thr
 100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Arg Arg Met Glu Lys
 115 120 125

Leu Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
 130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Val Asp Ala
 145 150 155 160

Val Asn Ile Pro Val Ile Gly Ala Gly Gly Val Ala Asp Gly Arg Gly
 165 170 175

Ala Ala Ala Val Phe Met Leu Gly Ala Glu Ala Ile Gln Val Gly Thr
 180 185 190

Arg Phe Ala Val Ala Lys Glu Ser Asn Ala His Ala Asn Phe Lys Lys
 195 200 205
 Lys Ile Leu Lys Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Ser Ile
 210 215 220
 Val Gly His Pro Val Arg Ala Ile Lys His Lys Leu Ser Ser Ala Tyr
 225 230 235 240
 Ala Thr Ala Glu Lys Glu Phe Leu Arg Gly Glu Lys Ser Gln Glu Asp
 245 250 255
 Ile Glu Val Leu Gly Ala Gly Ala Leu Arg Asn Ala Val Val Asp Gly
 260 265 270
 Asp Val Asp Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Phe Val
 275 280 285
 Thr Lys Glu Glu Thr Cys Glu Glu Ile Leu Lys Asp Leu Tyr Tyr Gly
 290 295 300
 Ala Ala Lys Val Ile Lys Ala Glu Ala Ala Arg Trp Ala Asp Val Glu
 305 310 315 320
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 <211> 972
 <212> DNA
 <213> Streptococcus pyogenes
 <400> 5
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 aagtatatgg aaagactgca ccaggcgggt ataatcggtt ttccgtgtgt cccaagcggt 360
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 gtttcgatcc ctgtcattgc ggcaggtggt atagctgatg gtcattggtgc agcagcagca 540
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gctaagcag aaaaagcatt ttttaattggt caaaaaacag ctactgatat tgaagaaatg      780
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<210> 6
<211> 323
<212> PRT
<213> Streptococcus pyogenes

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<400> 6

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Met Lys Thr Arg Ile Thr Glu Leu Leu Asn Ile Asp Tyr Pro Ile Phe
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Gln Gly Gly Met Ala Trp Val Ala Asp Gly Asp Leu Ala Gly Ala Val
20          25          30

Ser Asn Ala Gly Gly Leu Gly Ile Ile Gly Gly Gly Asn Ala Pro Lys
35          40          45

Glu Val Val Lys Ala Asn Ile Asp Arg Val Lys Ala Ile Thr Asp Arg
50          55          60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile
65          70          75          80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
85          90          95

Gly Asn Pro Gly Lys Tyr Met Glu Arg Leu His Gln Ala Gly Ile Ile
100         105         110

Val Val Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys
115         120         125

Leu Gly Val Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
130         135         140

Ile Gly Lys Leu Thr Thr Met Ser Leu Val Arg Gln Val Val Glu Ala
145         150         155         160

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Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly His Gly
165 170 175

Ala Ala Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Ile Gly Thr
180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Gln Asn Phe Lys Asp
195 200 205

Lys Ile Leu Ala Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Gln Val
210 215 220

Val Gly His Pro Val Arg Ser Ile Lys Asn Lys Leu Thr Ser Ala Tyr
225 230 235 240

Ala Lys Ala Glu Lys Ala Phe Leu Ile Gly Gln Lys Thr Ala Thr Asp
245 250 255

Ile Glu Glu Met Gly Ala Gly Ser Leu Arg His Ala Val Ile Glu Gly
260 265 270

Asp Val Val Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Val
275 280 285

Arg Lys Glu Glu Ser Cys Glu Thr Ile Leu Lys Asp Ile Tyr Tyr Gly
290 295 300

Ala Ala Arg Val Ile Gln Asn Glu Ala Lys Arg Trp Gln Ser Val Ser
305 310 315 320

Ile Glu Lys

<210> 7

<211> 1068

<212> DNA

<213> Staphylococcus aureus COL

<400> 7

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ggcacaatag ggcagaggta ctttaatacag cagcaattgg aagatgaat agattatgta 180

cgccaattaa cgtcaaatc ttttggcgta aatgtctttg taccaagtca acaatcatat 240

accagtagtc aaattgaaaa tatgaatgca tgggttaaac cttatcgacg cgcattacat 300

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ataagcaggt tgaagcagc gaatgtcaaa cttataggt cagcaacaag tgttgatgaa 480
gctattgcga atgaaaaagc gggtaggt gctatcgttg ctcaaggtag tgaagcaggt 540
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ttagtccac aaattgtaga tgcgtttca attccggtca ttgccgttg tggaattatg 660
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gcatttttaa catcacaaga cagtaatgca tcagaactac tgcgagatgc aattataaat 780
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atacatatgt ggagtgga aagcccgcca ctagcaacaa cgcattccgc caacaccatc 1020
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<210> 8
<211> 355
<212> PRT
<213> Staphylococcus aureus COL
<400> 8

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Met Trp Asn Lys Asn Arg Leu Thr Gln Met Leu Ser Ile Glu Tyr Pro
1          5          10          15

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Ile Ile Gln Ala Gly Met Ala Gly Ser Thr Thr Pro Lys Leu Val Ala
          20          25          30

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Ser Val Ser Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe
          35          40          45

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Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr
          50          55          60

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Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr
65          70          75          80

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Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg
          85          90          95

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Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln
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Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val
 115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu
 130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu
 145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly
 165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln
 180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val
 195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly
 210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr
 225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp
 245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe
 260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met
 275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu
 290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu
 305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro
 325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met
 340 345 350

Gln Tyr Lys
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<210> 9
<211> 999
<212> DNA
<213> *Enterococcus faecalis*

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tcattagcaa gtgcctgtgc aaacgctggg ggattagggg ttattgtctgg cggcaatgcc 180
ccaaaagaag tcgtaaaaaa agaaattaaa aaagttaaag aattaacgga gcaacccttt 240
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gaacagggtc ctgtcgtaac gacagggtgca ggcaatccag ccaaatatcat ggctcgtttt 360
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<210> 10
<211> 332
<212> PRT
<213> *Enterococcus faecalis*

<400> 10

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20 25 30

Gly Met Ala Trp Val Ala Asp Ala Ser Leu Ala Ser Ala Val Ser Asn
 35 40 45
 Ala Gly Gly Leu Gly Ile Ile Ala Gly Gly Asn Ala Pro Lys Glu Val
 50 55 60
 Val Lys Lys Glu Ile Lys Lys Val Lys Glu Leu Thr Glu Gln Pro Phe
 65 70 75 80
 Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Glu Ile Val Asp
 85 90 95
 Leu Val Cys Glu Glu Gln Val Pro Val Val Thr Thr Gly Ala Gly Asn
 100 105 110
 Pro Ala Lys Tyr Met Ala Arg Phe Lys Glu His Asn Ile Lys Val Ile
 115 120 125
 Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys Ile Gly
 130 135 140
 Ala Asp Ala Val Ile Phe Glu Gly Met Glu Ala Gly Gly His Ile Gly
 145 150 155 160
 Lys Leu Thr Thr Met Ser Gly Leu Pro Gln Ile Val Asp Ala Val Ser
 165 170 175
 Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg Gly Met Ala
 180 185 190
 Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Leu Gly Thr Arg Phe
 195 200 205
 Leu Ile Ala Lys Glu Cys Asn Val His Pro Asp Tyr Lys Gln Lys Val
 210 215 220
 Leu Lys Ala Arg Asp Leu Asp Ala Val Ile Thr Cys Gln His Phe Gly
 225 230 235 240
 His Pro Val Arg Thr Leu Lys Asn Lys Leu Thr Ala Gln Tyr Asn Gln
 245 250 255
 Leu Glu Lys Gln Glu Leu Gln Lys Glu Val Pro Asp Leu Glu Met Phe
 260 265 270
 Glu Lys Ile Gly Gln Gly Ala Leu Arg Lys Ala Val Val Asp Gly Asp

275

280

285

Met Asp Tyr Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Lys
 290 295 300

Lys Glu Glu Thr Ala Gln Glu Ile Ile Asp Ser Leu Met Ser Glu Cys
 305 310 315 320

Lys Ala Ile Val His Lys Met Asn Gln Arg Trp Gly
 325 330

<210> 11
 <211> 933
 <212> DNA
 <213> Clostridium acetobutylicum

<400> 11
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 ataatagcag cagcaaatgc accagttgag tatgtaagag atgaaataag gaaggcaaaa 180
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 gaagcagtag aagttataga tagaataaa tag 933

<210> 12
 <211> 310
 <212> PRT
 <213> Clostridium acetobutylicum
 <400> 12

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20 25 30

Val Ser Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Ala Asn Ala Pro
35 40 45

Val Glu Tyr Val Arg Asp Glu Ile Arg Lys Ala Lys Lys Leu Thr Asp
50 55 60

Lys Pro Phe Gly Val Asn Ile Met Leu Leu Ser Asp Asn Ala Glu Glu
65 70 75 80

Val Ala Lys Met Val Cys Glu Glu Gly Val Lys Val Val Thr Thr Gly
85 90 95

Ala Gly Asn Pro Gly Lys Tyr Ile Asp Met Trp Lys Glu His Asp Ile
100 105 110

Lys Val Ile Pro Val Val Ala Ser Val Ala Leu Ala Arg Arg Met Glu
115 120 125

Arg Cys Gly Val Asp Ala Val Val Ala Glu Gly Cys Glu Ser Gly Gly
130 135 140

His Val Gly Glu Leu Thr Thr Met Ala Leu Val Pro Gln Val Val Asp
145 150 155 160

Ala Ile Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg
165 170 175

Gly Val Ala Ala Phe Ala Leu Gly Ala Ser Gly Val Gln Val Gly
180 185 190

Thr Arg Phe Leu Ile Ala Lys Glu Cys Thr Val His Gln Asn Tyr Lys
195 200 205

Asn Lys Val Leu Lys Ala Lys Asp Ile Asp Thr Glu Val Thr Gly Arg
210 215 220

Ser Thr Gly His Pro Val Arg Val Leu Arg Asn Lys Leu Ala Arg Lys
225 230 235 240

Tyr Lys Leu Met Glu Lys Glu Gly Ala Ser Pro Glu Glu Met Glu Glu

Leu Gly Arg Gly Ala Leu Pro Arg Ala Val Arg Glu Gly Asp Val Asp
260 265 270

Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Asn Lys Glu
275 280 285

Glu Thr Cys Asp Glu Ile Val Glu Ser Met Phe Lys Glu Ala Val Glu
290 295 300

Val Ile Asp Arg Ile Lys
305 310

<210> 13
<211> 930
<212> DNA
<213> Clostridium difficile

<400> 13
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gcagcaggaa acgcacaaaa agaagctata aagaagaaa ttgttgagtg taaaaaatta 180
acagataaac cttttggagt aaatgtaatg cttatgtcgc catttggtga tgatataatt 240
gatttgatta tagaagaaaa agttcaagtt attactactg gtgctggaaa tcttgcaaaag 300
tatatggata gattaagga agctggaaca aagggttattc ctgtagtacc tacaatagct 360
ttggcacaaa gaattggaaa gctaggagct acagcagtaa tagcagaagg tactgaaggt 420
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aacatacctg taatagctgc tggaggaatt gtagatgga gaggaattgc agcatcattt 540
gcattaggtg ccagtgagcgt tcaagtagga actagattta ttgtagtgta agagtgttct 600
gtccattcaa actataaaaa cttagtacta aaagcaaaag atagagatgc aattgtaaca 660
ggaagaagta ctggtcatcc agtaagaaca ttaaaaaata aactatcaaa agaattttta 720
aagatggaac aaaaaggagc tactcctgaa gaattggata aaaaaggtag aggagcttta 780
agatttgcaa cagtagatgg agacatagaa aaagggtcat ttatggcagg tcaaatgtct 840
gctatggtaa aagaataaac accttgtaag gaaattatag aggcattagt aatcaagca 900
agagagatta tgccagcaat agaactgtaa 930

<210> 14
<211> 309
<212> PRT

<213> Clostridium difficile

<400> 14

Met Asn Lys Ile Cys Lys Ile Leu Asn Ile Lys Tyr Pro Val Ile Gln
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Gly Gly Met Ala Trp Val Ala Thr Ala Ser Leu Ala Ser Ala Val Ser
 20 25 30

Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Gly Asn Ala Pro Lys Glu
 35 40 45

Ala Ile Lys Lys Glu Ile Val Glu Cys Lys Lys Leu Thr Asp Lys Pro
 50 55 60

Phe Gly Val Asn Val Met Leu Met Ser Pro Phe Val Asp Asp Ile Ile
 65 70 75 80

Asp Leu Ile Ile Glu Glu Lys Val Gln Val Ile Thr Thr Gly Ala Gly
 85 90 95

Asn Pro Ala Lys Tyr Met Asp Arg Leu Lys Glu Ala Gly Thr Lys Val
 100 105 110

Ile Pro Val Val Pro Thr Ile Ala Leu Ala Gln Arg Met Glu Lys Leu
 115 120 125

Gly Ala Thr Ala Val Ile Ala Glu Gly Thr Glu Gly Gly Gly His Ile
 130 135 140

Gly Glu Leu Thr Thr Met Val Leu Val Pro Gln Val Ala Asp Ala Val
 145 150 155 160

Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Val Asp Gly Arg Gly Ile
 165 170 175

Ala Ala Ser Phe Ala Leu Gly Ala Ser Ala Val Gln Val Gly Thr Arg
 180 185 190

Phe Ile Cys Ser Glu Glu Cys Ser Val His Ser Asn Tyr Lys Asn Leu
 195 200 205

Val Leu Lys Ala Lys Asp Arg Asp Ala Ile Val Thr Gly Arg Ser Thr
 210 215 220

Gly His Pro Val Arg Thr Leu Lys Asn Lys Leu Ser Lys Glu Phe Leu

225

230

235

240

Lys Met Glu Gln Asn Gly Ala Thr Pro Glu Glu Leu Asp Lys Lys Gly
245 250 255

Thr Gly Ala Leu Arg Phe Ala Thr Val Asp Gly Asp Ile Glu Lys Gly
260 265 270

Ser Phe Met Ala Gly Gln Ser Ala Ala Met Val Lys Glu Ile Thr Pro
275 280 285

Cys Lys Glu Ile Ile Glu Ala Met Val Asn Gln Ala Arg Glu Ile Met
290 295 300

Pro Ala Ile Glu Leu
305

<210> 15

<211> 873

<212> DNA

<213> Porphyromonas gingivalis W83

<400> 15

atgaatagaa ttgtcggaatt attgggtatc gaacatccga tcatatcggg aggcattggtg 60
tggtgcagcg gttggaaact ggcttctgct gtgagcaact gcggtggttt gggacttatt 120
ggtgcoggat ccatgcattc ggacaatctg gagcatcaca tccgttcgtg taaagctgct 180
acagacaagc ctttcggtgt gaacgtgcct cttctctatc cggagatgga caaaatcatg 240
gagattatca tgagggaaca tgtgcccgta gtggtaacgt cagccggtag tccaaaggtg 300
tgacagacca agttgaaagc tgccggtagc aaggtgatac atgtagttag cagtggccaca 360
ttcgctcgca aatcagagcg agccggtgta gacgccatcg tggccgaagg gttcgaagcc 420
ggcgacata atggacgaga ggagactacg accctctggt tgatacctga agtagtggat 480
gctgtgaaca ttccctgggt tgctgccgga gggattgctt ccggccgtgc agttgccgct 540
gcttgggctt tgggtgcgga tgccgtacaa gtggggaccc gttttgctct gagtgaggaa 600
agttcggcgc atgaagactt taaggcacat tgccgccggt cgggtggagg agatacgtg 660
cttctgctca aggtctgtat ccctacgcga ctgctgaaga acaaattcta tcaggatgta 720
ttcgctgcgc agcagcgcggt tgcttcggtg gaagagctgc gcgagctgct cggtcgtggt 780
cgtgccaaagc aaggtatttt cgaaggcgac ctgcacgagg gcgaattgga gataggccag 840
gcagtatcgc agataagtca tgcggagacg gtg 873

<210> 16

<211> 313
 <212> PRT
 <213> Porphyromonas gingivalis W83

<400> 16

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Met Asn Arg Ile Cys Glu Leu Leu Gly Ile Glu His Pro Ile Ile Ser
1           5           10           15

Gly Gly Met Val Trp Cys Ser Gly Trp Lys Leu Ala Ser Ala Val Ser
20           25           30

Asn Cys Gly Gly Leu Gly Leu Ile Gly Ala Gly Ser Met His Pro Asp
35           40           45

Asn Leu Glu His His Ile Arg Ser Cys Lys Ala Ala Thr Asp Lys Pro
50           55           60

Phe Gly Val Asn Val Pro Leu Leu Tyr Pro Glu Met Asp Lys Ile Met
65           70           75           80

Glu Ile Ile Met Arg Glu His Val Pro Val Val Val Thr Ser Ala Gly
85           90           95

Ser Pro Lys Val Trp Thr Ala Lys Leu Lys Ala Ala Gly Ser Lys Val
100          105          110

Ile His Val Val Ser Ser Ala Thr Phe Ala Arg Lys Ser Glu Ala Ala
115          120          125

Gly Val Asp Ala Ile Val Ala Glu Gly Phe Glu Ala Gly Gly His Asn
130          135          140

Gly Arg Glu Glu Thr Thr Leu Cys Leu Ile Pro Glu Val Val Asp
145          150          155          160

Ala Val Asn Ile Pro Val Val Ala Ala Gly Gly Ile Ala Ser Gly Arg
165          170          175

Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Asp Ala Val Gln Val Gly
180          185          190

Thr Arg Phe Ala Leu Ser Glu Glu Ser Ser Ala His Glu Asp Phe Lys
195          200          205

Ala His Cys Arg Arg Ser Val Glu Gly Asp Thr Met Leu Ser Leu Lys
210          215          220

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Ala Val Ser Pro Thr Arg Leu Leu Lys Asn Lys Phe Tyr Gln Asp Val
225 230 235 240

Phe Ala Ala Glu Gln Arg Gly Ala Ser Val Glu Glu Leu Arg Glu Leu
245 250 255

Leu Gly Arg Gly Arg Ala Lys Gln Gly Ile Phe Glu Gly Asp Leu His
260 265 270

Glu Gly Glu Leu Glu Ile Gly Gln Ala Val Ser Gln Ile Ser His Ala
275 280 285

Glu Thr Val Ala Glu Ile Met Val Asp Leu Val Asp Gly Tyr Lys Arg
290 295 300

Ser Leu Ala Gly Met Pro Thr Glu Ile
305 310

<210> 17
<211> 966
<212> DNA
<213> *Caulobacter crescentus*

<400> 17
atgggcctgc gcaagccgct gtgtgatctg ctgggatatcg agcatccgat cctgctggcc 60
ggcatggggc ggggtctccta cgcgccgctg gccgccgccc tctccaacgc cggcggctat 120
ggcgtcctgg gcattggccg caccagcccg gacttcaccc gcgccacagat gcgcgaggtc 180
aaaagcctga ccgacaaacc gttcgggggtg gacctgctgg ccgccacgcg ggatgcgctg 240
accgcgtccg tccaggtcat catcgaggag ggccgcctcct catttgtcgc gggcctgggc 300
gtccccctgc ccatcatcga acgactcaag gccgccggcc tgaaggtcat ggtcgtctgc 360
ggagccgtga agcagccggt caaggccgag caggcgggct gcgaagcggt gatctgccaa 420
ggcggcgagg gcgggtgtca caccggtctc gtccgcaccc tgcgcgtgtg ggcgcaggcc 480
gtggaggcgg tgaagatccc ggtggtcggc gccggcgccc tgcgatcagg ccgcgggctg 540
gcggcgggcc tggctctggg gcgcgagggc gtctggatgg gcacgcgggt catcgccctg 600
cacgaggccc atcgggcgga tctctaccgc caggcgggtg tccaggccgc cgacgaggac 660
acggtgcgca cgcgctgcta ctccggcaag ccgatgcggg tgaagaagaa ccctatgtc 720
gacgactggg aagcgcgtcc cggcgacatc cagcccttcc cgcagcaggc catggtctcg 780
atccgcaatg gcgccatggg cggcatcggc gccagatcg agggcctgga cgcggccaag 840
tcctgcttcg ccatgggcca gagcgccggc ggcgtgcgag agatcttggc ggcggcgag 900

atcggtcaagc ggctgatggc cgaggccgag acggcgctgg ccaaggcctc ggccttcagg 960
 acctga 966

<210> 18
 <211> 321
 <212> PRT
 <213> Caulobacter crescentus

<400> 18

Met Gly Leu Arg Thr Pro Leu Cys Asp Leu Leu Asp Ile Glu His Pro
 1 5 10 15

Ile Leu Leu Ala Gly Met Gly Gly Val Ser Tyr Ala Pro Leu Ala Ala
 20 25 30

Ala Val Ser Asn Ala Gly Gly Tyr Gly Val Leu Gly Met Ala Gly Thr
 35 40 45

Ser Pro Asp Phe Ile Arg Ala Gln Met Arg Glu Val Lys Ser Leu Thr
 50 55 60

Asp Lys Pro Phe Gly Val Asp Leu Leu Ala Ala Thr Pro Asp Ala Leu
 65 70 75 80

Thr Ala Ser Val Glu Val Ile Ile Glu Glu Gly Ala Ser Ser Phe Val
 85 90 95

Ala Gly Leu Gly Val Pro Leu Pro Ile Ile Glu Arg Leu Lys Ala Ala
 100 105 110

Gly Leu Lys Val Met Val Val Cys Gly Ala Val Lys His Ala Val Lys
 115 120 125

Ala Glu Gln Ala Gly Cys Asp Ala Val Ile Cys Gln Gly Gly Glu Gly
 130 135 140

Gly Gly His Thr Gly Leu Val Gly Thr Leu Pro Leu Val Ala Gln Ala
 145 150 155 160

Val Glu Ala Val Lys Ile Pro Val Val Ala Ala Gly Gly Leu His Asp
 165 170 175

Gly Arg Gly Leu Ala Ala Ala Leu Ala Leu Gly Ala Gln Gly Val Trp
 180 185 190

Met Gly Thr Arg Phe Ile Ala Ser His Glu Ala His Ala Gly Asp Leu

Tyr Arg Gln Ala Val Val Glu Ala Ala Asp Glu Asp Thr Val Arg Thr
210 215 220

Arg Cys Tyr Ser Gly Lys Pro Met Arg Val Lys Lys Asn Pro Tyr Val
225 230 235 240

Asp Asp Trp Glu Ala Arg Pro Gly Asp Ile Gln Pro Phe Pro Gln Gln
245 250 255

Ala Met Val Ser Ile Arg Asn Gly Ala Met Gly Gly Ile Gly Gln
260 265 270

Ile Glu Gly Leu Asp Ala Ala Lys Ser Cys Phe Ala Met Gly Gln Ser
275 280 285

Ala Gly Gly Val Arg Glu Ile Leu Pro Ala Gly Glu Ile Val Lys Arg
290 295 300

Leu Met Ala Glu Ala Glu Thr Ala Leu Ala Lys Ala Ser Ala Phe Arg
305 310 315 320

Thr

<210> 19
<211> 987
<212> DNA
<213> *Pseudomonas aeruginosa*

<400> 19
atggcgctgt tcaggaccgc ttccaccgag accttcggcg tcgaacaccc gatcatgcag 60
ggcgcatgc agtgggtcgg ccgtgccgag atggctcggc cggtgccaa cgccggtggc 120
ctggcgacgc tctcggcgtt gaccacgcgc agcccgagg cactggctgc ggagattgcc 180
cgctgccgag agctgacoga tcggccgttc ggggtcaacc tgaccttgc gccagcgag 240
aagccggtgc cctatgcoga atatcgcgca gccatcatcg aggcgggaat ccgctcgtc 300
gaaacgcgcg gcaacgaccc cggcgagcac atcgccgaat tccgtcgaca cggcgtcaag 360
gtgatccaca agtgcaaccg cgtgcgccat gcgctcaagg ccgagcgact gggcgtggac 420
gcgctctcca tcgacggctt cgagtgtgcc ggccaccgag gcgaggacga catccccggc 480
ctggtgtgtc tgccggcgcg ggccaaccgg ctacgcgtgc cgatcatcgc ctccggcggt 540
ttcgccgatg gacgtggcct ggtcgcggcg ctggcgctgg gtgccgacgc gatcaacatg 600

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ggcacgcgct tcttggccac tgcgaatgt ccgatacacc ctgcgggtgaa ggccggcgatc 660
cgtgcgggccc acgagcgcttc caccgacctg atcatgcgtt cccctgcgcaa taccggcgcg 720
gtggcgcgca acgcgatcag ccaggaagta ctggcgatcg aggcacgcgg cgccggccggc 780
tacgccgata tgcgccgctt ggtcagcggc cagcgcggtc gccaggtgta ccagcagggc 840
gataccgacc tggggatctg gtcggccggc atggtccagg gcctgatcga cgacgaaccg 900
gcctgcgccc agttgctcag gacatcgtc gacgaggcgc gccaaactggt gcgtcaacgc 960
ctggagggca tgctcgccgg ggtctga 987

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<210> 20
<211> 328
<212> PRT
<213> Pseudomonas aeruginosa

```

```

<400> 20

```

```

Met Gly Val Phe Arg Thr Arg Phe Thr Glu Thr Phe Gly Val Glu His
1 5 10 15

```

```

Pro Ile Met Gln Gly Gly Met Gln Trp Val Gly Arg Ala Glu Met Ala
20 25 30

```

```

Ala Ala Val Ala Asn Ala Gly Gly Leu Ala Thr Leu Ser Ala Leu Thr
35 40 45

```

```

Gln Pro Ser Pro Glu Ala Leu Ala Ala Glu Ile Ala Arg Cys Arg Glu
50 55 60

```

```

Leu Thr Asp Arg Pro Phe Gly Val Asn Leu Thr Leu Leu Pro Thr Gln
65 70 75 80

```

```

Lys Pro Val Pro Tyr Ala Glu Tyr Arg Ala Ala Ile Ile Glu Ala Gly
85 90 95

```

```

Ile Arg Val Val Glu Thr Ala Gly Asn Asp Pro Gly Glu His Ile Ala
100 105 110

```

```

Glu Phe Arg Arg His Gly Val Lys Val Ile His Lys Cys Thr Ala Val
115 120 125

```

```

Arg His Ala Leu Lys Ala Glu Arg Leu Gly Val Asp Ala Val Ser Ile
130 135 140

```

```

Asp Gly Phe Glu Cys Ala Gly His Pro Gly Glu Asp Asp Ile Pro Gly
145 150 155 160

```

Leu Val Leu Leu Pro Ala Ala Ala Asn Arg Leu Arg Val Pro Ile Ile
165 170 175

Ala Ser Gly Gly Phe Ala Asp Gly Arg Gly Leu Val Ala Ala Leu Ala
180 185 190

Leu Gly Ala Asp Ala Ile Asn Met Gly Thr Arg Phe Leu Ala Thr Arg
195 200 205

Glu Cys Pro Ile His Pro Ala Val Lys Ala Ala Ile Arg Ala Ala Asp
210 215 220

Glu Arg Ser Thr Asp Leu Ile Met Arg Ser Leu Arg Asn Thr Ala Arg
225 230 235 240

Val Ala Arg Asn Ala Ile Ser Gln Glu Val Leu Ala Ile Glu Ala Arg
245 250 255

Gly Gly Ala Gly Tyr Ala Asp Ile Ala Leu Val Ser Gly Gln Arg
260 265 270

Gly Arg Gln Val Tyr Gln Gln Gly Asp Thr Asp Leu Gly Ile Trp Ser
275 280 285

Ala Gly Met Val Gln Gly Leu Ile Asp Asp Glu Pro Ala Cys Ala Glu
290 295 300

Leu Leu Arg Asp Ile Val Glu Gln Ala Arg Gln Leu Val Arg Gln Arg
305 310 315 320

Leu Glu Gly Met Leu Ala Gly Val
325

<210> 21
<211> 1044
<212> DNA
<213> Bacillus subtilis

<400> 21
atgaatgaat ttatgaaaaa gttttcttta acaaaaccca ttattcaagc tccaatggct 60
ggcgggtatta caaagccccc acttgcatct gcagtttcga atcaagggtc tcttggcagc 120
ttagcatcgg ggtattcttac gccagacctc ctagaacaac' aaataaaaga aatatttgag 180
ctgacagacg ctccctttta aattaatgtg ttgttccgc taggtctaga gatgccacca 240
aaagatcaga ttaaaaaagt gaaagaaaac ataccgtag ctaatcaagt aaatcaattc 300

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acatctgtac aagaagagtg ggaatgacttc tatcaaaaaa ttgatctaataa tttaaaaatac 360
aagggttaag cttgctcatt cacttttggat ctgcccgcctg aagacgcagt aaaggagcta 420
aaaaccgctg gatgctgttt aataggaacc gttcaacag tagaagaagc attgttaatg 480
gaagaacggg gaattgatat agtagtcctt caaggaagtg aagccgggtg acatcgcgga 540
gcattcttac cttccaaagg tgaatctgcc gtaggttttaa tggctctgat tccacaagca 600
gcagatgcac tgacgtgacc tgcataagct gctgggggaa tgaatagacca cagaggagta 660
aaagcagctt taaccctcgg agcccaaggc gttcaaatcg gttctgcctt ttttaattgt 720
cacgagagta acgcacatcc agtcataaa cagaaaatac tagaagcaaa cgaagcagat 780
acaaagctta cgacattatt ttcaggtaaa gaggccagag gaatcgtaaa taaatggatg 840
gaagaaaatg aacagtttga gacacaaacc cttccgtacc cttatcaaaa tacactaacg 900
aaggcaatga gacagaaggc ttcacttcaa aataaccatg atcagatgtc tttatgggca 960
ggtcaaggga tacggtcatt gactgaggaa atttcgggta agcagctttt aaatcagctt 1020
tgccaagagg atataaaaat atag 1044

```

```

<210> 22
<211> 347
<212> PRT
<213> Bacillus subtilis
<400> 22

```

```

Met Asn Glu Phe Met Lys Lys Phe Ser Leu Thr Lys Pro Ile Ile Gln
1 5 10 15

```

```

Ala Pro Met Ala Gly Gly Ile Thr Lys Pro Arg Leu Ala Ser Ala Val
20 25 30

```

```

Ser Asn Gln Gly Ala Leu Gly Ser Leu Ala Ser Gly Tyr Leu Thr Pro
35 40 45

```

```

Asp Leu Leu Glu Gln Gln Ile Lys Glu Ile Phe Glu Leu Thr Asp Ala
50 55 60

```

```

Pro Phe Gln Ile Asn Val Phe Val Pro Leu Gly Leu Glu Met Pro Pro
65 70 75 80

```

```

Lys Asp Gln Ile Lys Lys Trp Lys Glu Asn Ile Pro Leu Ala Asn Gln
85 90 95

```

```

Val Asn Gln Phe Thr Ser Val Gln Glu Glu Trp Asp Asp Phe Tyr Gln
100 105 110

```

Lys Ile Asp Leu Ile Leu Lys Tyr Lys Val Lys Ala Cys Ser Phe Thr
 115 120 125

Phe Asp Leu Pro Pro Glu Asp Ala Val Lys Glu Leu Lys Thr Ala Gly
 130 135 140

Cys Cys Leu Ile Gly Thr Ala Ser Thr Val Glu Glu Ala Leu Leu Met
 145 150 155 160

Glu Glu Arg Gly Met Asp Ile Val Val Leu Gln Gly Ser Glu Ala Gly
 165 170 175

Gly His Arg Gly Ala Phe Leu Pro Ser Lys Gly Glu Ser Ala Val Gly
 180 185 190

Leu Met Ala Leu Ile Pro Gln Ala Ala Asp Ala Leu Ser Val Pro Val
 195 200 205

Ile Ala Ala Gly Gly Met Ile Asp His Arg Gly Val Lys Ala Ala Leu
 210 215 220

Thr Leu Gly Ala Gln Gly Val Gln Ile Gly Ser Ala Phe Leu Ile Cys
 225 230 235 240

His Glu Ser Asn Ala His Pro Val His Lys Gln Lys Ile Leu Glu Ala
 245 250 255

Asn Glu Ala Asp Thr Lys Leu Thr Thr Leu Phe Ser Gly Lys Glu Ala
 260 265 270

Arg Gly Ile Val Asn Lys Trp Met Glu Glu Asn Glu Gln Phe Glu Thr
 275 280 285

Gln Thr Leu Pro Tyr Pro Tyr Gln Asn Thr Leu Thr Lys Ala Met Arg
 290 295 300

Gln Lys Ala Ser Leu Gln Asn Asn His Asp Gln Met Ser Leu Trp Ala
 305 310 315 320

Gly Gln Gly Ile Arg Ser Leu Thr Glu Glu Ile Ser Val Lys Gln Leu
 325 330 335

Leu Asn Gln Leu Cys Gln Glu Asp Ile Lys Ile
 340 345

<210> 23
 <211> 1128
 <212> DNA
 <213> *Mycobacterium tuberculosis* rv1533

<400> 23
 atgctggacca gactcgccga gctgctcggg gctgagtttc caatatgcgc gttcagccac 60
 tgccgggatg tgggtggcggc ggtgtccaat gcgggcccggg tcgggatctc cgggtgcgctc 120
 gcacatagcc ccaaacggct ggagagcgag ctgacctgga tcgaggagca cacgggtggc 180
 aagccgtacg gactcgacgt gctgctgccg cccaatata tcggcgccga gcaaggcggg 240
 atcgatgcc agcaggcccg ggagctcata cccgaagggc atcgacactt cgtcgacgac 300
 ttgctgggtc gctatggcat ccccgcggtc accgacccgc agcgttcgtc ctggcgccgt 360
 gggctgcaca tctcgcccaa gggttatcag ccgttctgtg atgtggcctt cgcccatgac 420
 atccggttga tcgccagcgc gctcggggcg ccgcaccggc atctcgtgga gcgcgcccac 480
 aaccatgacg tgcgtgggtg cgccttagcc ggacagggcg agcacgcgcg gcgacacgcg 540
 gctcgggggt ttgacctgat cgtcgcgagc ggacacgagg ccggaggcca caccggcgag 600
 gtggcgacca tggttctggt tccgaagtc gtcgatcgcg tgcgccaac gccggtgctg 660
 gcccgggcgc ggatcgcccg tggcgccag atcgctcgcg cgttggccct gggggcgga 720
 ggcgtctggt gcgggtcggg ctggttgacc accgaagaag ccgaaacgcc ccggtggtc 780
 aaggacaagt ttctggcgcg aacatcctcg gacacggtgc ggtcccggtc gctaaccggc 840
 aagccggcgc gcactgctgc cacggcctgg accgacgaat gggatcggcc tgacagcccc 900
 gaccgccttg gcactccgct gcagagcgcg ctggtcagcg acccgaggt gcgcatcaac 960
 caggcgccgc gccagcccg ggccaaggct cgtgagctgg cgacctactt cgtcggacag 1020
 gtcgtcggt cactcgaccg ggtcgggtcg gccgcctcgg tgggtcctga catggtcgag 1080
 gagtctatcg acacgctcg gcaactgcag ggggtggtgc aaaggtga 1128

<210> 24
 <211> 375
 <212> PRT
 <213> *Mycobacterium tuberculosis* rv1533

<400> 24
 Met Arg Thr Arg Val Ala Glu Leu Leu Gly Ala Glu Phe Pro Ile Cys
 1 5 10 15
 Ala Phe Ser His Cys Arg Asp Val Val Ala Ala Val Ser Asn Ala Gly
 20 25 30
 Gly Phe Gly Ile Leu Gly Ala Val Ala His Ser Pro Lys Arg Leu Glu

35

40

45

Ser Glu Leu Thr Trp Ile Glu Glu His Thr Gly Gly Lys Pro Tyr Gly
50 55 60

Val Asp Val Leu Leu Pro Pro Lys Tyr Ile Gly Ala Glu Gln Gly Gly
65 70 75 80

Ile Asp Ala Gln Gln Ala Arg Glu Leu Ile Pro Glu Gly His Arg Thr
85 90 95

Phe Val Asp Asp Leu Leu Val Arg Tyr Gly Ile Pro Ala Val Thr Asp
100 105 110

Arg Gln Arg Ser Ser Ser Ala Gly Gly Leu His Ile Ser Pro Lys Gly
115 120 125

Tyr Gln Pro Leu Leu Asp Val Ala Phe Ala His Asp Ile Arg Leu Ile
130 135 140

Ala Ser Ala Leu Gly Pro Pro Pro Asp Leu Val Glu Arg Ala His
145 150 155 160

Asn His Asp Val Leu Val Ala Ala Leu Ala Gly Thr Ala Gln His Ala
165 170 175

Arg Arg His Ala Ala Ala Gly Val Asp Leu Ile Val Ala Gln Gly Thr
180 185 190

Glu Ala Gly Gly His Thr Gly Glu Val Ala Thr Met Val Leu Val Pro
195 200 205

Glu Val Val Asp Ala Val Ser Pro Thr Pro Val Leu Ala Ala Gly Gly
210 215 220

Ile Ala Arg Gly Arg Gln Ile Ala Ala Ala Leu Ala Leu Gly Ala Glu
225 230 235 240

Gly Val Trp Cys Gly Ser Val Trp Leu Thr Thr Glu Glu Ala Glu Thr
245 250 255

Pro Pro Val Val Lys Asp Lys Phe Leu Ala Ala Thr Ser Ser Asp Thr
260 265 270

Val Arg Ser Arg Ser Leu Thr Gly Lys Pro Ala Arg Met Leu Arg Thr
275 280 285

Ala Trp Thr Asp Glu Trp Asp Arg Pro Asp Ser Pro Asp Pro Leu Gly
290 295 300

Met Pro Leu Gln Ser Ala Leu Val Ser Asp Pro Gln Leu Arg Ile Asn
305 310 315 320

Gln Ala Ala Gly Gln Pro Gly Ala Lys Ala Arg Glu Leu Ala Thr Tyr
325 330 335

Phe Val Gly Gln Val Val Gly Ser Leu Asp Arg Val Arg Ser Ala Arg
340 345 350

Ser Val Val Leu Asp Met Val Glu Glu Phe Ile Asp Thr Val Gly Gln
355 360 365

Leu Gln Gly Leu Val Gln Arg
370 375

<210> 25
<211> 1035
<212> DNA
<213> Mycobacterium tuberculosis rv2781c

<400> 25
atggtgttgg gcttctggga catcgcggtg ccatcgctcg gcgccccgat ggccggcggc 60
cagagcaacc cggcgttggc cgcggcggtg tccaacgctg gcgggcttgg tttcgtcgcc 120
ggcggctatc tgagcgcgga cgggctcgcc gacgatatcg ccgctgcgcg cgccgcoact 180
accggctcta tcggagcga tctgtttgtg ccccaaccca gcgtcgccga ctgggcgcag 240
ctggagtatt acgcggaaga gctcgaagag gtccgaggt actaccacac cgagggtggc 300
cagcccgctc atggtgacga cagcagctgg gtgcgcaaac tcgaggtggt agccgatgtt 360
cgtccggagg tgggtgcgtt cacttcggc gcgcgcgcgc cggatgtcgt gcagcggttg 420
agcgcgctgg gactgttggc ctcgatcacc gtgacgtcgg tctacgagcg cggtgtggcc 480
attgccgcgg gcgcggacag cctggtgggc cagggcccg gcgcgcgcgc gcacgcggga 540
acgttcgcgc cggacatgga acccggtacg gactcgctgc accaactcct cgatcggatt 600
ggcagcgccc atgatgtgcc gctggttgca gccggtggcc tgggcacggc tgaggacgtg 660
gccgcgctgc tgcgccgcgg agcgatcgcc gccaggttg gtaccgcatt gctgctggcc 720
gacgaagcgg gtaccaatgc cgcacaccgt gccgcgctga agaattccaga gttcgatgcc 780
accctggtca ctccggcggt ctccggtagg tatgcgcgcg gtctggccaa caacttcact 840
cgctgctcg accacgtggc gccgctgggt tatccggagg tccaccagat gacgaagcgg 900

atacgggagg cgagggtgca ggcggagac cgcacggaa caaacctttg ggcgggacg 960
 ggcacccgga agaccggcc gggaccggcg gccgacatca tcgttccct tactcccgac 1020
 gtgtgctcgg cgtaa 1035

<210> 26
 <211> 344
 <212> PRT
 <213> Mycobacterium tuberculosis rv2781c

<400> 26

Met Val Leu Gly Phe Trp Asp Ile Ala Val Pro Ile Val Gly Ala Pro
 1 5 10 15

Met Ala Gly Gly Pro Ser Thr Pro Ala Leu Ala Ala Val Ser Asn
 20 25 30

Ala Gly Gly Leu Gly Phe Val Ala Gly Gly Tyr Leu Ser Ala Asp Arg
 35 40 45

Leu Ala Asp Asp Ile Ala Ala Ala Arg Ala Ala Thr Gly Pro Ile
 50 55 60

Gly Ala Asn Leu Phe Val Pro Gln Pro Ser Val Ala Asp Trp Ala Gln
 65 70 75 80

Leu Glu Tyr Tyr Ala Asp Glu Leu Glu Glu Val Ala Glu Tyr Tyr His
 85 90 95

Thr Glu Val Gly Gln Pro Val Tyr Gly Asp Asp Asp Asp Trp Val Arg
 100 105 110

Lys Leu Glu Val Val Ala Asp Val Arg Pro Glu Val Val Ser Phe Thr
 115 120 125

Phe Gly Ala Pro Pro Pro Asp Val Val Gln Arg Leu Ser Ala Leu Gly
 130 135 140

Leu Leu Val Ser Ile Thr Val Thr Ser Val Tyr Glu Ala Gly Val Ala
 145 150 155 160

Ile Ala Ala Gly Ala Asp Ser Leu Val Val Gln Gly Pro Ala Ala Gly
 165 170 175

Gly His Arg Gly Thr Phe Ala Pro Asp Met Glu Pro Gly Thr Glu Ser
 180 185 190

Leu His Gln Leu Leu Asp Arg Ile Gly Ser Ala His Asp Val Pro Leu
195 200 205

Val Ala Ala Gly Gly Leu Gly Thr Ala Glu Asp Val Ala Ala Val Leu
210 215 220

Arg Arg Gly Ala Ile Ala Ala Gln Val Gly Thr Ala Leu Leu Leu Ala
225 230 235 240

Asp Glu Ala Gly Thr Asn Ala Ala His Arg Ala Ala Leu Lys Asn Pro
245 250 255

Glu Phe Asp Ala Thr Leu Val Thr Arg Ala Phe Ser Gly Arg Tyr Ala
260 265 270

Arg Gly Leu Ala Asn Asn Phe Thr Arg Leu Leu Asp His Val Ala Pro
275 280 285

Leu Gly Tyr Pro Glu Val His Gln Met Thr Lys Pro Ile Arg Ala Ala
290 295 300

Ala Val Gln Ala Asp Asp Pro His Gly Thr Asn Leu Trp Ala Gly Ser
305 310 315 320

Ala His Arg Lys Thr Arg Pro Gly Pro Ala Ala Asp Ile Ile Ala Ser
325 330 335

Leu Thr Pro Asp Val Cys Ser Ala
340

<210> 27
<211> 1068
<212> DNA
<213> Mycobacterium tuberculosis rv3553

<400> 27
atgaggctgc gtacgccgct gaccgagctc atcgccatcg agcacccggt ggtgcagacc 60
gggatgggct ggggtggcgg tgcccggtcg gtgtoggcca ccgccaaacg gggcgggctg 120
ggcatcttgg cctcggccac catgacgctg gacgagctgg cggcgggcga cacaaggctc 180
aaggccgtca ccgacaagcc attcgggggtg aacatccgcg ccgacgcagc cgacgcgggc 240
gaccgcgtcg agttgatgat ccgcgagggg gtgcgggtgg cctcgttcgc gttggcacc 300
aaacagcagc tgatcgcccc gctcaaagaa gccggcgcgg tggcgcatac gtcgatcggc 360
gcggccaaac atgcgcgcaa ggtggcgggc tggggcgccg acgcgatgat cgtgcagggc 420

```

ggcgaggggc gcgccacac cgggccggtc gccaccacgc tgcgttgcc gtcggtgctg      480
gacgcgcgtg cgggcaccgg catcccggtg atcgccgccg ggggcttctt cgcggggcgc      540
gggctagccg cggcggttggt ctacggcgcc gccgggggtg ccatgggcac cgggtttctg      600
ctcacctcgg attccacctg gcccgacgcg gtcaaacggc gttacctgca ggccggcttg      660
gacggcaccg tggtcaccac ccgcgtcgac gggatgccgc accgggtgct gcgcaccgag      720
ctggtcgaga agctggaaag cggtcgcgcg gcacgaggtt tcggggccgc gctgcgcaat      780
gccggcaagt ttacagcgat gtcgcagatg acctggcggt cgatgatccg agacggcctg      840
accatgcgcc acggcaagga attgacctgg tcacagggtg tgatggcggc aaacaccccg      900
atgctgctca aagccggcct ggtcgacggc aacaccgagg cgggggtgct ggcacgggc      960
caggtagcgg gcattcttga cgacctaccg tcgtgcaaag agctgatcga gtcgatcgtg     1020
cttgacgcca tcacacattt acaaacgcga tctgcgctgg tggagtga                     1068

```

```

<210> 28
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis rv3553
<400> 28

```

```

Met Arg Leu Arg Thr Pro Leu Thr Glu Leu Ile Gly Ile Glu His Pro
 1             5             10             15

```

```

Val Val Gln Thr Gly Met Gly Trp Val Ala Gly Ala Arg Leu Val Ser
      20             25             30

```

```

Ala Thr Ala Asn Ala Gly Gly Leu Gly Ile Leu Ala Ser Ala Thr Met
      35             40             45

```

```

Thr Leu Asp Glu Leu Ala Ala Ala Ile Thr Lys Val Lys Ala Val Thr
      50             55             60

```

```

Asp Lys Pro Phe Gly Val Asn Ile Arg Ala Asp Ala Ala Asp Ala Gly
      65             70             75             80

```

```

Asp Arg Val Glu Leu Met Ile Arg Glu Gly Val Arg Val Ala Ser Phe
      85             90             95

```

```

Ala Leu Ala Pro Lys Gln Gln Leu Ile Ala Arg Leu Lys Glu Ala Gly
      100            105            110

```

```

Ala Val Val Ile Pro Ser Ile Gly Ala Ala Lys His Ala Arg Lys Val
      115            120            125

```

Ala Ala Trp Gly Ala Asp Ala Met Ile Val Gln Gly Gly Glu Gly Gly
 130 135 140

Gly His Thr Gly Pro Val Ala Thr Thr Leu Leu Leu Pro Ser Val Leu
 145 150 155 160

Asp Ala Val Ala Gly Thr Gly Ile Pro Val Ile Ala Ala Gly Gly Phe
 165 170 175

Phe Asp Gly Arg Gly Leu Ala Ala Ala Leu Cys Tyr Gly Ala Ala Gly
 180 185 190

Val Ala Met Gly Thr Arg Phe Leu Leu Thr Ser Asp Ser Thr Val Pro
 195 200 205

Asp Ala Val Lys Arg Arg Tyr Leu Gln Ala Gly Leu Asp Gly Thr Val
 210 215 220

Val Thr Thr Arg Val Asp Gly Met Pro His Arg Val Leu Arg Thr Glu
 225 230 235 240

Leu Val Glu Lys Leu Glu Ser Gly Ser Arg Ala Arg Gly Phe Ala Ala
 245 250 255

Ala Leu Arg Asn Ala Gly Lys Phe Arg Arg Met Ser Gln Met Thr Trp
 260 265 270

Arg Ser Met Ile Arg Asp Gly Leu Thr Met Arg His Gly Lys Glu Leu
 275 280 285

Thr Trp Ser Gln Val Leu Met Ala Ala Asn Thr Pro Met Leu Leu Lys
 290 295 300

Ala Gly Leu Val Asp Gly Asn Thr Glu Ala Gly Val Leu Ala Ser Gly
 305 310 315 320

Gln Val Ala Gly Ile Leu Asp Asp Leu Pro Ser Cys Lys Glu Leu Ile
 325 330 335

Glu Ser Ile Val Leu Asp Ala Ile Thr His Leu Gln Thr Ala Ser Ala
 340 345 350

Leu Val Glu
 355

<210> 29
 <211> 969
 <212> DNA
 <213> Mycobacterium tuberculosis rv0021c

```

<400> 29
gtggtgcat cgacggcctt tagccagatg ttcggaatcg actatccgat agtgtccgcg      60
ccaatggact tgatgccggc cgggtgagctg gctgccgcgg taagtggcgc agggggactc      120
ggcctcatcg ggggcggcta tggggaccgg gattggttgg ccggcagatt cgatctcgcc      180
gctggagcgc cggtgggctg cgggttcac acctggtctt tggcccgcca accgcagctg      240
ctcgacctcg cgctgcagta tgagccgggtg gcggtgatgc tgcgttcgg ggaccccgcg      300
gttttcgctg acgccatcaa gtccgcggga acgcggttgg tctgccagat ccaaaaccgg      360
accaggcgcg agcagaccct gcaggtcggc gccgatgtgt tggtggtcca gggcaccgag      420
gccggtgggc acggccacgg tccacgttcc accctgacct tggtagccga aatcgtagac      480
ctggtcaccc cgccgggaac tgatatcccg gtgatcgccg ccgggggcat cgccgacggc      540
cggggccttg ccgcccgtt gatgttgggc gccgcggggg tattggtcgg tacgcgcttc      600
tacgccacgg tcgaagcgtt atccacaccg caggcgcggg acccgctgct ggcgcccaact      660
ggcgacgaca tgtgccgcac cactatctac gatcagctac ggcgctatcc ctggccgcaa      720
ggacacacga tgagcgtgct aagcaacgcc ctacccgacc aattcgagga caccgaactc      780
gacattctcc atcgcaaga agccatggcc agatattggc gagccgttgc tgcgcgtgac      840
tacagcatcg ccaatgtcac cgcgggtcaa gccgcggggc tggtaaatgc cgtcctgcca      900
gccgcgacg tgataaccgg tatggcgcaa caagcggcga ggacgctgac cgcgatgcgc      960
gccgtgttaa
  
```

<210> 30
 <211> 322
 <212> PRT
 <213> Mycobacterium tuberculosis rv0021c

<400> 30

```

Met Val Leu Ser Thr Ala Phe Ser Gln Met Phe Gly Ile Asp Tyr Pro
1           5           10          15
  
```

```

Ile Val Ser Ala Pro Met Asp Leu Ile Ala Gly Gly Glu Leu Ala Ala
          20          25          30
  
```

```

Ala Val Ser Gly Ala Gly Gly Leu Gly Leu Ile Gly Gly Gly Tyr Gly
          35          40          45
  
```


Asp Arg Asp Trp Leu Ala Arg Gln Phe Asp Leu Ala Ala Gly Ala Pro
 50 55 60

Val Gly Cys Gly Phe Ile Thr Trp Ser Leu Ala Arg Gln Pro Gln Leu
 65 70 75 80

Leu Asp Leu Ala Leu Gln Tyr Glu Pro Val Ala Val Met Leu Ser Phe
 85 90 95

Gly Asp Pro Ala Val Phe Ala Asp Ala Ile Lys Ser Ala Gly Thr Arg
 100 105 110

Leu Val Cys Gln Ile Gln Asn Arg Thr Gln Ala Glu Arg Ala Leu Gln
 115 120 125

Val Gly Ala Asp Val Leu Val Ala Gln Gly Thr Glu Ala Gly Gly His
 130 135 140

Gly His Gly Pro Arg Ser Thr Leu Thr Leu Val Pro Glu Ile Val Asp
 145 150 155 160

Leu Val Thr Ala Arg Gly Thr Asp Ile Pro Val Ile Ala Ala Gly Gly
 165 170 175

Ile Ala Asp Gly Arg Gly Leu Ala Ala Ala Leu Met Leu Gly Ala Ala
 180 185 190

Gly Val Leu Val Gly Thr Arg Phe Tyr Ala Thr Val Glu Ala Leu Ser
 195 200 205

Thr Pro Gln Ala Arg Asp Pro Leu Leu Ala Ala Thr Gly Asp Asp Met
 210 215 220

Cys Arg Thr Thr Ile Tyr Asp Gln Leu Arg Arg Tyr Pro Trp Pro Gln
 225 230 235 240

Gly His Thr Met Ser Val Leu Ser Asn Ala Leu Thr Asp Gln Phe Glu
 245 250 255

Asp Thr Glu Leu Asp Ile Leu His Arg Glu Glu Ala Met Ala Arg Tyr
 260 265 270

Trp Arg Ala Val Ala Ala Arg Asp Tyr Ser Ile Ala Asn Val Thr Ala
 275 280 285

Gly Gln Ala Ala Gly Leu Val Asn Ala Val Leu Pro Ala Ala Asp Val

290

295

300

Ile Thr Gly Met Ala Gln Gln Ala Ala Arg Thr Leu Thr Ala Met Arg
 305 310 315 320

Ala Val

```

<210> 31
<211> 1131
<212> DNA
<213> Mycobacterium tuberculosis rv1894c

<400> 31
atgcacactg ccatttgcca cgagctcggg atcgagtttc ctatttttgc cttcactcac      60
tgccgcgatg tgggtggtgc cgtcagcaaa gctggtggtt ttggtgtgct cggagcagtt      120
gggttcacgc cggagcagct ggagatcgag ctcaactgga tcgatgaaca catcggcgac      180
caccctacg gggctgacat cgtgatcccg aacaagtacg agggcatgga ctcccagctg      240
tcggcgggat agctcgccaa gacgctgcgg tcgatggtec cgcaggagca tctggacttc      300
gcccgcaaga tctcgcgca tcattggtgt ccggtcgagg acgccgacga ggacagtctg      360
cagctgtctg gttggaccga ggcgacggcc accccacagg tcgaocggcg gctgaagcac      420
cccaagatga cgatggtgc caacgcgctt ggccccccc cagcggacat gatcaagcac      480
atccacgact cgggtcgcaa ggtggccgca ttgtgcggct caccctcgca ggcccgcaag      540
caccgcgatg cgggcgtcga catcatcatc gccacggggc gcgagggccg cgggcactgt      600
ggcgaggtag gctccattgt gttgtggcct caggctcgta aggaggtagc gccggttcgc      660
gtgttgccgg cgggtggcat cggcagcggg cagcagatcg ctgcagcgtt gccgctgggg      720
acccaagggg catggaccgg ttgcagtggt ctgatggtcg aggaagccgc aaacaccgcg      780
gttcaacagg ccgcatacgt caaggcgacc agcccgacga ccgtgcgcga tcgttccttc      840
acgggttaag cggcccgcat gctgcgcaac gactggactg aggcctggga gcaaccggag      900
agcccgaaag cgctcggtat gccgttgcaa tacatggtct ccggcatggc cgtcaaagcc      960
acacataaat acccgaaaga gaccgtcgac gtgcggttca acccggtggg gcagggtgtt      1020
gggcagttca ccaagtgga aaagacgggt accgttatcg aacgctgggt gcaggagtag      1080
ctcagggcga ccgcccgggt ggacgcactc aatgctgcgc cgtccgtttg a      1131

<210> 32
<211> 376
<212> PRT
<213> Mycobacterium tuberculosis rv1894c

```

<400> 32

Met His Thr Ala Ile Cys Asp Glu Leu Gly Ile Glu Phe Pro Ile Phe
1 5 10 15

Ala Phe Thr His Cys Arg Asp Val Val Val Ala Val Ser Lys Ala Gly
20 25 30

Gly Phe Gly Val Leu Gly Ala Val Gly Phe Thr Pro Glu Gln Leu Glu
35 40 45

Ile Glu Leu Asn Trp Ile Asp Glu His Ile Gly Asp His Pro Tyr Gly
50 55 60

Val Asp Ile Val Ile Pro Asn Lys Tyr Glu Gly Met Asp Ser Gln Leu
65 70 75 80

Ser Ala Asp Glu Leu Ala Lys Thr Leu Arg Ser Met Val Pro Gln Glu
85 90 95

His Leu Asp Phe Ala Arg Lys Ile Leu Ala Asp His Gly Val Pro Val
100 105 110

Glu Asp Ala Asp Glu Asp Ser Leu Gln Leu Leu Gly Trp Thr Glu Ala
115 120 125

Thr Ala Thr Pro Gln Val Asp Ala Ala Leu Lys His Pro Lys Met Thr
130 135 140

Met Val Ala Asn Ala Leu Gly Thr Pro Pro Ala Asp Met Ile Lys His
145 150 155 160

Ile His Asp Ser Gly Arg Lys Val Ala Ala Leu Cys Gly Ser Pro Ser
165 170 175

Gln Ala Arg Lys His Ala Asp Ala Gly Val Asp Ile Ile Ile Ala Gln
180 185 190

Gly Gly Glu Ala Gly Gly His Cys Gly Glu Val Gly Ser Ile Val Leu
195 200 205

Trp Pro Gln Val Val Lys Glu Val Ala Pro Val Pro Val Leu Ala Ala
210 215 220

Gly Gly Ile Gly Ser Gly Gln Gln Ile Ala Ala Ala Leu Ala Leu Gly
225 230 235 240

Thr Gln Gly Ala Trp Thr Gly Ser Gln Trp Leu Met Val Glu Glu Ala
245 250 255

Ala Asn Thr Ala Val Gln Gln Ala Ala Tyr Val Lys Ala Thr Ser Arg
260 265 270

Asp Thr Val Arg Ser Arg Ser Phe Thr Gly Lys Pro Ala Arg Met Leu
275 280 285

Arg Asn Asp Trp Thr Glu Ala Trp Glu Gln Pro Glu Ser Pro Lys Pro
290 295 300

Leu Gly Met Pro Leu Gln Tyr Met Val Ser Gly Met Ala Val Lys Ala
305 310 315 320

Thr His Lys Tyr Pro Asn Glu Thr Val Asp Val Ala Phe Asn Pro Val
325 330 335

Gly Gln Val Val Gly Gln Phe Thr Lys Val Glu Lys Thr Ala Thr Val
340 345 350

Ile Glu Arg Trp Val Gln Glu Tyr Leu Glu Ala Thr Ala Arg Leu Asp
355 360 365

Ala Leu Asn Ala Ala Ala Ser Val
370 375

<210> 33

<211> 945

<212> DNA

<213> *Thermotoga maritima*

<400> 33

atgaccgtga gaacaagagt gacagatctt ctggaaatag agcatccaat cctcatgggt 60

ggaatggcct gggcggaac tcccaccctc gcagcagcgg tatcggaggg gggaggactt 120

ggaatcatcg gatccggagc catgaagcgg gacgacctga gaaaagcgat ctccgaactc 180

agacagaaga cggacaaacc ctccggtgta aacataatcc ttgtctctcc gtgggcggac 240

gatctcgtca aggtgtgcat agaagagaaa gtaccgctcg tcacgttcgg tgcgggaaac 300

ccaacgaagt acataaggga actcaaggaa aacggaacaa aggtgatacc cgttgtcgcc 360

tccgactctc tggcaaggat ggtggaaga gcgggagcgg atcgggtgat agcgggaagg 420

atggagtcgg gtggacacat aggtgaagtc acaaccttcg ttctcgtcaa caaagtctcc 480

aggagtgtga acatccccgt gatcgacggc ggaggcatcg ccgacggaag aggtatggca 540

gccgccttcg cactcggagc ggaagccgtt cagatgggaa ccaggtttgt ggcgagtgtg 600
 gaaagcgacg tgcacccggt ttacaaagaa aagatcgta aggttccat aagagacacc 660
 gttgtgacgg gagccaaact tggacacccc gcgcgcgttc tcagaactcc ctttgaagg 720
 aagatccagg agatggagtt tgaacacccc atgcaggctg aagaaatgct ggtgggaagt 780
 ctcaagaagag cggtcgttga aggcgatctg gagagaggat ccttcatggt gggacagagc 840
 gccggcttga tcgatgatgat aaaaccggtg aagcagatca tagaggatat cctgaaggag 900
 ttcaaagaaa cgggtggagaa gctgaggggg tacatcgaag agtga 945

<210> 34
 <211> 314
 <212> PRT
 <213> Thermotoga maritima

<400> 34

Met Thr Val Arg Thr Arg Val Thr Asp Leu Leu Glu Ile Glu His Pro
1 5 10 15

Ile Leu Met Gly Gly Met Ala Trp Ala Gly Thr Pro Thr Leu Ala Ala
20 25 30

Ala Val Ser Glu Ala Gly Gly Leu Gly Ile Ile Gly Ser Gly Ala Met
35 40 45

Lys Pro Asp Asp Leu Arg Lys Ala Ile Ser Glu Leu Arg Gln Lys Thr
50 55 60

Asp Lys Pro Phe Gly Val Asn Ile Ile Leu Val Ser Pro Trp Ala Asp
65 70 75 80

Asp Leu Val Lys Val Cys Ile Glu Glu Lys Val Pro Val Val Thr Phe
85 90 95

Gly Ala Gly Asn Pro Thr Lys Tyr Ile Arg Glu Leu Lys Glu Asn Gly
100 105 110

Thr Lys Val Ile Pro Val Val Ala Ser Asp Ser Leu Ala Arg Met Val
115 120 125

Glu Arg Ala Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ser Gly
130 135 140

Gly His Ile Gly Glu Val Thr Thr Phe Val Leu Val Asn Lys Val Ser
145 150 155 160

Arg Ser Val Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly
165 170 175

Arg Gly Met Ala Ala Ala Phe Ala Leu Gly Ala Glu Ala Val Gln Met
180 185 190

Gly Thr Arg Phe Val Ala Ser Val Glu Ser Asp Val His Pro Val Tyr
195 200 205

Lys Glu Lys Ile Val Lys Ala Ser Ile Arg Asp Thr Val Val Thr Gly
210 215 220

Ala Lys Leu Gly His Pro Ala Arg Val Leu Arg Thr Pro Phe Ala Arg
225 230 235 240

Lys Ile Gln Glu Met Glu Phe Glu Asn Pro Met Gln Ala Glu Glu Met
245 250 255

Leu Val Gly Ser Leu Arg Arg Ala Val Val Glu Gly Asp Leu Glu Arg
260 265 270

Gly Ser Phe Met Val Gly Gln Ser Ala Gly Leu Ile Asp Glu Ile Lys
275 280 285

Pro Val Lys Gln Ile Ile Glu Asp Ile Leu Lys Glu Phe Lys Glu Thr
290 295 300

Val Glu Lys Leu Arg Gly Tyr Ile Glu Glu
305 310

<210> 35

<211> 1092

<212> DNA

<213> Helicobacter pylori

<400> 35

atggtatcaa cactcaaac gctaaaaatc ggtaaacaca ccataaaatt ccctattttt 60

caagggggca tgggtgtggg gattagctgg gatgaactag ctggaaatgt tgccaaagaa 120

ggggcttttag gagtgatttc agccgtaggc actggttatt ataaaaacat gcgttttcta 180

gaaaggattg tggctaaaaa accctttgaa gccttgaatt ttactccaa aaaagcgttg 240

aatgagattt ttgcaaacgc taggaaaatt tgcgggaaca agcctttggg ggccaatatt 300

ttatcgccta tcaatgacta tggccgtgtt ttaagggact cttgtgaggc gggggcgaa 360

attatcatta caggggctgg ttgcccact aacatgcctg aattcgctaa ggatttttag 420

```

gatgtggcgc tcatccctat catttccctca gcgaaggcct taaaaatcct ttgtaaaaga 480
tggagcgcgc gctataaaaag aatcccgagc gcattcattg tggaggggcc tttgagtgagg 540
gggcacacagg gctttaaaata cgaagattgt ttcaagaag aattccaatt agaaaactta 600
gtgcctaaaag tcgtggaagc ttctaaagaa tgggggaata tccctatcat cgccgcgggg 660
gggatattggg ataagaaga tatagacacc atgttaagcc ttggagcgag tgggggtgcaa 720
atggcgactc gttttttagg cacgaaagaa tgcgacgcta aagcgtatgc cgatcttttg 780
cccacgctca aaaaagaaga tattttactc atcaaatcgc ctgtaggcta tccggctagg 840
gctatcaata cgggggtgat caaacgcatt gaagagggtta acgcgctaa aatcgcatgc 900
gtgagcaatt gtgtagcgcc ttgtaacagg ggtgaagaag ctaaaaaggt gggctattgt 960
atcgctgatg gtttggggcg cagttattta ggaacagag aagaggggct ttttttacc 1020
ggggctaata gctatagagt ggataagatt atcagcgtgc atgaattgat taaagagcct 1080
acagagggtt aa 1092

```

```

<210> 36
<211> 363
<212> PRT
<213> Helicobacter pylori
<400> 36

```

```

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys
1 5 10 15

```

```

Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu
20 25 30

```

```

Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala
35 40 45

```

```

Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val
50 55 60

```

```

Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu
65 70 75 80

```

```

Asn Glu Ile Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu
85 90 95

```

```

Gly Ala Asn Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg
100 105 110

```

```

Asp Ser Cys Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu

```

115	120	125
Pro Thr Asn Met	Pro Glu Phe Ala Lys Asp Phe Ser Asp Val Ala Leu	
130	135	140
Ile Pro Ile Ile Ser Ser Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg		
145	150	155
Trp Ser Asp Arg Tyr Lys Arg Ile Pro Asp Ala Phe Ile Val Glu Gly		
	165	170
Pro Leu Ser Gly Gly His Gln Gly Phe Lys Tyr Glu Asp Cys Phe Lys		
	180	185
Glu Glu Phe Gln Leu Glu Asn Leu Val Pro Lys Val Val Glu Ala Ser		
	195	200
Lys Glu Trp Gly Asn Ile Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp		
	210	215
Lys Lys Asp Ile Asp Thr Met Leu Ser Leu Gly Ala Ser Gly Val Gln		
	225	230
Met Ala Thr Arg Phe Leu Gly Thr Lys Glu Cys Asp Ala Lys Ala Tyr		
	245	250
Ala Asp Leu Leu Pro Thr Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys		
	260	265
Ser Pro Val Gly Tyr Pro Ala Arg Ala Ile Asn Thr Gly Val Ile Lys		
	275	280
Arg Ile Glu Glu Gly Asn Ala Pro Lys Ile Ala Cys Val Ser Asn Cys		
	290	295
Val Ala Pro Cys Asn Arg Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys		
	305	310
Ile Ala Asp Gly Leu Gly Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly		
	325	330
Leu Tyr Phe Thr Gly Ala Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser		
	340	345
Val His Glu Leu Ile Lys Glu Leu Thr Glu Gly		
	355	360

<210> 37
 <211> 825
 <212> DNA
 <213> Archaeoglobus fulgidus

```

<400> 37
atgaacaggga ttgctaaact cctcaaaacg aagtatccga tagttcaggg cccgatggcc      60
ggaataaactc tcggagaatt tgcttctaca gtgtctgagg ctggcgggct tggagttata      120
gcttctgccc gcttctgccg tgaaaaaacta aaagaggaga tagagaaagt taagaacagg      180
actgataagc ccttcgccgt gaacattcca atatatcagc cgggctcgga gaagaatctt      240
gagactgcac ttaaagctga tgttgggatt atttacacct ctgcaggaag cccggagaaaa      300
tacactgaga gagtaaagga atccggggca aaagtcatac acaaggtgtc gaggttgaaa      360
gaggggctga aagcggagaa ggcgggagtg gatgctgtgg ttgcgatggg ctttgaggcg      420
ggaggggatta tagggaggag tgggtgaaca tccttctgct tgattctcga gcttgcgcac      480
aacctcagca ttccagtgtg agccgctggc gggatagcag atgagagggg atttgctgca      540
gccttgattc tcggagcgga aggtgttgag attggcacga gactgcttgc aaccaagag      600
tgcccgctgc cggaaagcat taagcaagct attttaaaag ccacctcgca ctccacgatg      660
gttattgaga gcccggttgt aatgagagct ctcaagccag agctgagcgg agattctgag      720
aatcctgctc tgggagggca ggtttcaggg ctgattaagg agattcttac ggttgaagag      780
gtaatcagga aaattgcaga ggggctgaat aaagctaaat tctaa                        825

```

<210> 38
 <211> 274
 <212> PRT
 <213> Archaeoglobus fulgidus

<400> 38

```

Met Asn Arg Ile Ala Lys Leu Leu Lys Thr Lys Tyr Pro Ile Val Gln
1           5           10          15

```

```

Gly Pro Met Ala Gly Ile Thr Leu Gly Glu Phe Ala Ser Thr Val Ser
          20          25          30

```

```

Glu Ala Gly Gly Leu Gly Val Ile Ala Ser Ala Gly Leu Ser Pro Glu
35          40          45

```

```

Lys Leu Lys Glu Glu Ile Glu Lys Val Lys Asn Arg Thr Asp Lys Pro
50          55          60

```

```

Phe Ala Val Asn Ile Pro Ile Tyr Gln Pro Gly Ser Glu Lys Asn Leu

```

```
<210> 39
<211> 1125
<212> DNA
<213> Willliopsis saturnus
<400> 39
```

```

atgagatcac aaatacagag cttcctaaag acgtttgaag tcaggatccc tattattcac      60
gccccaatgg ctggcgcttc gaccttgaa ctcgcagcca ccgtaaccag actcggaggc      120
attggttcga tccctatggg ctgcctgagt gagaagtgtg atgctattga gacccagctg      180
gaaaattttg atgaattggt tggtgattct ggaaggatag tcaacttgaa cttctttgct      240
cataaggagc ctgcttctgg gagagctgat gtaacgagg aatggctcaa gaagtatgac      300
aagatatatg gcaaagccgg aattgagttt gacaaaaagg agctgaagtt gttatatcca      360
tcttttaggt ccattgttga tccacaacat ccgactgtgc ggctactgaa gaatctcaag      420
ccaaagattg tcagtttcca ctttgggtta ccccatgagg cggtgattga atctctccag      480
gcaagcgata ttaagatctt tgtcactgtc acaaatctac aggagtttca gcaggcttat      540
gagtctaaat tggatggtgt cgtcctacaa ggatgggaag ctgggggaca tcgtggtaat      600
ttcaaggcta atgacgtcga agatggacaa ctgaagacgt tggatctcgt tagtactatt      660
gttgattaca ttgactcggc tagtatctcc aatccacat ttatcattgc agcgggtggt      720
attcatgatg atgagtcgat caaagaattg cttcaattca acattgtgc cgttcagttg      780
ggctactgtt ggttaccatc gagccaggcc acaatatctc ctgaacattt gaagatgttt      840
caatcccaa aaagtgcac gatgatgacc gcagccattt caggacgtaa cttgagaacg      900
atcagtacac ctttcttgag ggatcttcat caatcttcac cattggcctc gatccctgat      960
tatccattac cttacgacag ctttaagtca cttgctaata acgctaagca aagtggaataa      1020
gggcctcagt actcgcgatt tcttgctgga tctaactatc acaaatcttg gaaggatagc      1080
agatccactg aagagatatt ctgatatta gtacaggatc tataa                        1125

```

```

<210> 40
<211> 374
<212> PRT
<213> Williopsis saturnus

```

```

<400> 40

```

```

Met Arg Ser Gln Ile Gln Ser Phe Leu Lys Thr Phe Glu Val Arg Tyr
1           5           10          15

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Pro Ile Ile Gln Ala Pro Met Ala Gly Ala Ser Thr Leu Glu Leu Ala
20          25          30

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Ala Thr Val Thr Arg Leu Gly Gly Ile Gly Ser Ile Pro Met Gly Ser
35          40          45

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Leu Ser Glu Lys Cys Asp Ala Ile Glu Thr Gln Leu Glu Asn Phe Asp
50          55          60

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Glu Leu Val Gly Asp Ser Gly Arg Ile Val Asn Leu Asn Phe Phe Ala
65 70 75 80

His Lys Glu Pro Arg Ser Gly Arg Ala Asp Val Asn Glu Glu Trp Leu
85 90 95

Lys Lys Tyr Asp Lys Ile Tyr Gly Lys Ala Gly Ile Glu Phe Asp Lys
100 105 110

Lys Glu Leu Lys Leu Leu Tyr Pro Ser Phe Arg Ser Ile Val Asp Pro
115 120 125

Gln His Pro Thr Val Arg Leu Leu Lys Asn Leu Lys Pro Lys Ile Val
130 135 140

Ser Phe His Phe Gly Leu Pro His Glu Ala Val Ile Glu Ser Leu Gln
145 150 155 160

Ala Ser Asp Ile Lys Ile Phe Val Thr Val Thr Asn Leu Gln Glu Phe
165 170 175

Gln Gln Ala Tyr Glu Ser Lys Leu Asp Gly Val Val Leu Gln Gly Trp
180 185 190

Glu Ala Gly Gly His Arg Gly Asn Phe Lys Ala Asn Asp Val Glu Asp
195 200 205

Gly Gln Leu Lys Thr Leu Asp Leu Val Ser Thr Ile Val Asp Tyr Ile
210 215 220

Asp Ser Ala Ser Ile Ser Asn Pro Pro Phe Ile Ile Ala Ala Gly Gly
225 230 235 240

Ile His Asp Asp Glu Ser Ile Lys Glu Leu Leu Gln Phe Asn Ile Ala
245 250 255

Ala Val Gln Leu Gly Thr Val Trp Leu Pro Ser Ser Gln Ala Thr Ile
260 265 270

Ser Pro Glu His Leu Lys Met Phe Gln Ser Pro Lys Ser Asp Thr Met
275 280 285

Met Thr Ala Ala Ile Ser Gly Arg Asn Leu Arg Thr Ile Ser Thr Pro
290 295 300

Phe Leu Arg Asp Leu His Gln Ser Ser Pro Leu Ala Ser Ile Pro Asp
305 310 315 320

Tyr Pro Leu Pro Tyr Asp Ser Phe Lys Ser Leu Ala Asn Asp Ala Lys
325 330 335

Gln Ser Gly Lys Gly Pro Gln Tyr Ser Ala Phe Leu Ala Gly Ser Asn
340 345 350

Tyr His Lys Ser Trp Lys Asp Thr Arg Ser Thr Glu Glu Ile Phe Ser
355 360 365

Ile Leu Val Gln Asp Leu
370

<210> 41

<211> 1215

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 41

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cctatggcgg gggtcacgac tattgaaatg gccgctaagg ctgttattgc gggcgccata 180
gcttcactac cctatcccca cttagacttc agaaaggcca atgatattga aaagcttaaa 240
ctgatggttt cacaattcag agatcaagta gccgatgaat ctttagaggg caatctcaac 300
ctaaactttt ttgcccata tatcgttgat aaaccgaccg atcttcaaac agctaactgg 360
gcgaagctat acagaaaagtc tatgaatgtg ccgattgata tgaatgagat taaattogat 420
aatggtaaat tatcttttaa ggcatttgaa aaagaaaatg ctcttcaaga ttttttcag 480
tacctatcag atggcttttag gcctaaaatc attagtcttc attttgccca tccgtcgaaa 540
tctacaatag aatatattaca aaaaattgga attctaattt ttgtgactgc cacctctgta 600
agagaagttc gattgttagc acgtctcggc attaatggca tagtgtgtca aggcctatgaa 660
gcgggaggac atagaggaaa tttcttagta aatgacccca aagatgatga aaacttatca 720
actgtacaat tgggtgaaaag aacagttgat gaacttgctg aaatgaaaaa taaaggctctt 780
atacatgcta ctccctttgt cattgcagca ggtggtataa tggattccaa agatatatca 840
tacatgttat cacagcaagc agacgtgtgt caagtgggga ctgcttttct tgggtgcagt 900
gaatccaatg catcaaaaaa cttttcaagc ccttcactc gagaacaac aactaaaatg 960
gttaataata tatcaggaaa gcctgcaagg accatctcta ctccctttat cgaaaaagtc 1020
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caagtaagaa aaaagtatcc agaattggct aactttattt tagctggaca aggatttcag 1140
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attgtcggaa aataa 1215

<210> 42
<211> 404
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 42

Met Tyr Phe Leu Asn Gln Leu Ile Phe Gln Asp Val Ser Val Met Ser
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Val Asp Lys Arg Glu Asp Met Ser Arg Ser Phe Gln Lys Cys Leu Asn
20 25 30

Leu Arg Tyr Pro Ile Ile Gln Ala Pro Met Ala Gly Val Thr Thr Ile
35 40 45

Glu Met Ala Ala Lys Ala Cys Ile Ala Gly Ala Ile Ala Ser Leu Pro
50 55 60

Leu Ser His Leu Asp Phe Arg Lys Val Asn Asp Ile Glu Lys Leu Lys
65 70 75 80

Leu Met Val Ser Gln Phe Arg Asp Gln Val Ala Asp Glu Ser Leu Glu
85 90 95

Gly Asn Leu Asn Leu Asn Phe Phe Cys His Asp Ile Val Asp Lys Pro
100 105 110

Thr Asp Leu Gln Thr Ala Asn Trp Ala Lys Leu Tyr Arg Lys Ser Met
115 120 125

Asn Val Pro Ile Asp Met Asn Glu Ile Lys Phe Asp Asn Gly Asn Val
130 135 140

Ser Phe Lys Ala Phe Glu Lys Glu Asn Ala Leu Gln Asp Phe Phe Gln
145 150 155 160

Tyr Leu Ser Asp Gly Phe Arg Pro Lys Ile Ile Ser Phe His Phe Gly
165 170 175

His Pro Ser Lys Ser Thr Ile Glu Tyr Leu Gln Lys Ile Gly Ile Leu
180 185 190

Ile Phe Val Thr Ala Thr Ser Val Arg Glu Val Arg Leu Leu Ala Arg
195 200 205

Leu Gly Ile Asn Gly Ile Val Cys Gln Gly Tyr Glu Ala Gly Gly His
210 215 220

Arg Gly Asn Phe Leu Val Asn Asp Pro Lys Asp Asp Glu Asn Leu Ser
225 230 235 240

Thr Val Gln Leu Val Lys Arg Thr Val Asp Glu Leu Ala Glu Met Lys
245 250 255

Asn Lys Gly Leu Ile His Ala Thr Pro Phe Val Ile Ala Ala Gly Gly
260 265 270

Ile Met Asp Ser Lys Asp Ile Ser Tyr Met Leu Ser Gln Gln Ala Asp
275 280 285

Ala Val Gln Val Gly Thr Ala Phe Leu Gly Cys Ser Glu Ser Asn Ala
290 295 300

Ser Lys Asn Phe Ser Ser Pro Phe Thr Arg Glu Thr Thr Thr Lys Met
305 310 315 320

Val Asn Ile Ile Ser Gly Lys Pro Ala Arg Thr Ile Ser Thr Pro Phe
325 330 335

Ile Glu Lys Val Ile Ala Asn Phe Gln Gly Glu Glu Leu Pro Tyr
340 345 350

Gly Tyr Met Tyr Ser Ala Phe Lys Gln Val Arg Lys Lys Tyr Pro Glu
355 360 365

Leu Ala Asn Phe Ile Leu Ala Gly Gln Gly Phe Gln Asn Val Gln Ser
370 375 380

Gly Ile Thr Thr Asp Lys Lys Ile Glu Thr Met Gly Ala Arg Leu Lys
385 390 395 400

Ile Val Gly Lys

<210> 43
<211> 1137
<212> DNA

<213> *Neurospora crassa*

<400> 43
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 atcgccaacg gcactcttgc ggccgaggtg tccaaggccg gcggtattgg ctttgtcgcc 180
 ggcggctcgc acttccgcgc cggtctctcc caccataacg cctctctac cgaactcgcc 240
 tccgcccgca gccgcctcgg tcttaccgac cgccectca cctctctccc cggtattggc 300
 gtcggcctca ttttaaccca caccatctcc gttccctacg taaccgacac cgtctgccc 360
 atcctgatcg aacactcccc gcaagcagtc tggctcttcg ccaacgaccc ggatttcgag 420
 gcctcttcgc agcctggcgc aaaggaaca gcaaagcaaa tcacgagggc ccttcacgct 480
 tcggggttcg tggattctt tcaagtaggc acggtgaaag atgcaaggaa ggcggcggca 540
 gatggggcag atgtgattgt tgcgcaaggg atcgatgcgg gagggcatca gcttgctaca 600
 gggagtggga ttgtgagttt ggtaccggag gttagggata tgcttgatag agagttcaag 660
 gaacgagagg tgggtggtgt ggcggcggga ggtgtggcgg atgggagggg ggttgtaggg 720
 gcgctgggtc taggcgcgca ggggtgtgta ttgggtacta ggttcaccgt agcagtcgaa 780
 gcttccaccc ccgagttcgc cagggaaggtc atcctcgaga caaacgatgg tggctcgaac 840
 accgtcaaat cccatttcca cgaccaaata aactgcaaca caatctggca caacgtctac 900
 gacggcgag ccgttcgcaa tgctctctac gacgaccacg cggccggtgt cccctttgaa 960
 gagaatcaca agaagttcaa ggaggcagcg agctctgggg ataactcgcg ggcgtgact 1020
 tgggtccggga ctgctgtggg tctgataaag gaccagaggg cggtcgcgca tattgttagg 1080
 gaggtagggg aagaggccaa agagaggatc aagaagattc aggcctttgc tgcttaa 1137

<210> 44

<211> 378

<212> PRT

<213> *Neurospora crassa*

<400> 44

Met His Phe Pro Gly His Ser Ser Lys Lys Glu Glu Ser Ala Gln Ala
 1 5 10 15

Ala Leu Thr Lys Leu Asn Ser Trp Phe Pro Thr Thr Lys Asn Pro Val
 20 25 30

Ile Ile Ser Ala Pro Met Tyr Leu Ile Ala Asn Gly Thr Leu Ala Ala
 35 40 45

Glu Val Ser Lys Ala Gly Gly Ile Gly Phe Val Ala Gly Gly Ser Asp
 50 55 60

Phe Arg Pro Gly Ser Ser His Leu Thr Ala Leu Ser Thr Glu Leu Ala
 65 70 75 80

Ser Ala Arg Ser Arg Leu Gly Leu Thr Asp Arg Pro Leu Thr Pro Leu
 85 90 95

Pro Gly Ile Gly Val Gly Leu Ile Leu Thr His Thr Ile Ser Val Pro
 100 105 110

Tyr Val Thr Asp Thr Val Leu Pro Ile Leu Ile Glu His Ser Pro Gln
 115 120 125

Ala Val Trp Leu Phe Ala Asn Asp Pro Asp Phe Glu Ala Ser Ser Glu
 130 135 140

Pro Gly Ala Lys Gly Thr Ala Lys Gln Ile Ile Glu Ala Leu His Ala
 145 150 155 160

Ser Gly Phe Val Val Phe Phe Gln Val Gly Thr Val Lys Asp Ala Arg
 165 170 175

Lys Ala Ala Ala Asp Gly Ala Asp Val Ile Val Ala Gln Gly Ile Asp
 180 185 190

Ala Gly Gly His Gln Leu Ala Thr Gly Ser Gly Ile Val Ser Leu Val
 195 200 205

Pro Glu Val Arg Asp Met Leu Asp Arg Glu Phe Lys Glu Arg Glu Val
 210 215 220

Val Val Val Ala Ala Gly Gly Val Ala Asp Gly Arg Gly Val Val Gly
 225 230 235 240

Ala Leu Gly Leu Gly Ala Glu Gly Val Val Leu Gly Thr Arg Phe Thr
 245 250 255

Val Ala Val Glu Ala Ser Thr Pro Glu Phe Arg Arg Lys Val Ile Leu
 260 265 270

Glu Thr Asn Asp Gly Gly Leu Asn Thr Val Lys Ser His Phe His Asp
 275 280 285

Gln Ile Asn Cys Asn Thr Ile Trp His Asn Val Tyr Asp Gly Arg Ala

290

295

300

Val Arg Asn Ala Ser Tyr Asp Asp His Ala Ala Gly Val Pro Phe Glu
 305 310 315 320

Glu Asn His Lys Lys Phe Lys Glu Ala Ala Ser Ser Gly Asp Asn Ser
 325 330 335

Arg Ala Val Thr Trp Ser Gly Thr Ala Val Gly Leu Ile Lys Asp Gln
 340 345 350

Arg Pro Ala Gly Asp Ile Val Arg Glu Leu Arg Glu Glu Ala Lys Glu
 355 360 365

Arg Ile Lys Lys Ile Gln Ala Phe Ala Ala
 370 375

<210> 45

<211> 195

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabK Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X=Ile or Ala

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> X=any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> X=Gly or Ala

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> X=Gly or Pro

<220>

<221> MISC_FEATURE

<222> (8)..(16)

<223> X=any amino acid and up to 3 may be absent

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<220>
<221> MISC_FEATURE
<222> (18)..(19)
<223> X=Pro, Ala, Gly, Ser or Thr

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> X=Ser or Ala

<220>
<221> MISC_FEATURE
<222> (22)..(23)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (26)..(53)
<223> X=any amino acid and up to 6 may be absent

<220>
<221> MISC_FEATURE
<222> (55)..(55)
<223> X=Gln, Asn, Glu or Asp

<220>
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<222> (56)..(56)
<223> X=any amino acid

<220>
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<222> (59)..(59)
<223> X=Gly or Ala

<220>
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<222> (61)..(165)
<223> X=any amino acid and up to 15 may be absent

<220>
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<222> (167)..(168)
<223> X=Ile or Val

<220>
<221> MISC_FEATURE
<222> (169)..(169)
<223> X=Ala or Gly

<220>

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<221> MISC_FEATURE
<222> (170)..(170)
<223> X=Ala or Ser

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<220>
<221> MISC_FEATURE
<222> (173)..(180)
<223> X=any amino acid

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<220>
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<222> (182)..(182)
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<220>
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<222> (183)..(183)
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<220>
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<222> (184)..(184)
<223> X=any amino acid

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<220>
<221> MISC_FEATURE
<222> (188)..(192)
<223> X=any amino acid

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<400> 45

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Pro Xaa Xaa Xaa Xaa Xaa Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1          5          10          15

```

```

Ala Xaa Xaa Val Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20          25          30

```

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35          40          45

```

```

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Pro Phe Xaa Val Xaa Xaa Xaa Xaa
50          55          60

```

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65          70          75          80

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```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85          90          95

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 145 150 155 160

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa
 165 170 175

Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Leu Gly Ala Xaa Xaa Xaa Xaa Xaa
 180 185 190

Gly Thr Arg
 195

<210> 46

<211> 60

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabK Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X=Ile or Val

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> X=any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> X=Gly or Ala

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> X=Gly or Pro

<220>

<221> MISC_FEATURE
 <222> (8)..(16)
 <223> X=any amino acid and up to 3 may be absent

<220>
 <221> MISC_FEATURE
 <222> (18)..(19)
 <223> X=Pro, Ala, Gly, Ser, or Thr

<220>
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 <222> (21)..(21)
 <223> X=Ser or Ala

<220>
 <221> MISC_FEATURE
 <222> (22)..(23)
 <223> X=any amino acid

<220>
 <221> MISC_FEATURE
 <222> (26)..(53)
 <223> X=any amino acid and up to 6 may be absent

<220>
 <221> MISC_FEATURE
 <222> (55)..(55)
 <223> X=Gln, Asn, Glu, or Asp

<220>
 <221> MISC_FEATURE
 <222> (56)..(56)
 <223> X=any amino acid

<220>
 <221> MISC_FEATURE
 <222> (59)..(59)
 <223> X=Gly or Ala

<400> 46

Pro Xaa Xaa Xaa Xaa Xaa Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Ala Xaa Xaa Val Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Pro Phe Xaa Val
50 55 60

<210> 47
<211> 1167
<212> DNA
<213> Staphylococcus aureus NCTC 8325

<400> 47
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actcaaatgt taagtattga atatccaatt attacagcag gtttggcagg aagtacgacc 180
cccaaattag ttgcattaat taataacagt ggtgggttag gcacaatagg cgcaggttac 240
tttaatacgc agcaattgga agatgaaata gattatgtac gccaatatc gtcgaattct 300
tttggcgtaa atgtctttgt accaagtcaa caatcatata ccagtagtca aattgaaaat 360
atgaatgcat gggtaaaacc ttatcgacgc gcattacatt tagaagagcc gggtgtaaaa 420
attaccgaag aacaacaatt taagtgtcat attgatacga taattaaaaa gcaagtgcct 480
gtatgttgtt ttacttttgg aattccaagc gaacagatta taagcagggt gaaagcagcg 540
aatgtcaaac ttataggtac agcaacaagt gttgatgaag ctattgcgaa tgaaaaagcg 600
ggatgtgatg ctatcgttgc tcaaggtagt gaagcagggt gacatcgtgg ttcattttta 660
aaacctaaaa atcaattacc tatggttgga acaatatctt tagtgccaca aattgtagat 720
gtcgtttcaa ttccggtcat tgccgctggt ggaattatgg atggttagagg agttttggca 780
agtattgtct taggtgcaga aggggtacaa atgggcaccg catttttaac atcacaagac 840
agtaatgcat cagaactact gcgagatgca attataaata gtaagaaac agatacagtc 900
attacaaaag cgtttagtgg aaagcttgca cgcggtatca acaataggtt tatogaagaa 960
atgtcccaat acgaaggcga tatccagat tatccaatac aaaaatgagct aacaagtagc 1020
ataagaaaag cgcgagcaaa catcggcgac aaagagttaa tacatatgtg gagtggacaa 1080
agcccgcgac tagcaacaac gcattccgcc aacaccatca tgtccaatat aatcaatcaa 1140
attaatcaaa tcatgcaata taaataa 1167

<210> 48
<211> 355
<212> PRT
<213> Staphylococcus aureus NCTC 8325

<400> 48

Met Trp Asn Lys Asn Arg Leu Thr Gln Met Leu Ser Ile Glu Tyr Pro
1 5 10 15

Ile Ile Thr Ala Gly Leu Ala Gly Ser Thr Thr Pro Lys Leu Val Ala
 20 25 30

Leu Ile Asn Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe
 35 40 45

Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr
 50 55 60

Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr
 65 70 75 80

Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg
 85 90 95

Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln
 100 105 110

Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val
 115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu
 130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu
 145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly
 165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln
 180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val
 195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly
 210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr
 225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp
 245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe
260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met
275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu
290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu
305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro
325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met
340 345 350

Gln Tyr Lys
355

<210> 49

<211> 753

<212> DNA

<213> FabI Bacillus subtilis

<400> 49

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gcgatcagac ttgctgagaa cggctataac atcgtcatta actatgcacg cagcaaaaaa	120
gcagcattag aaacagcggg agaaatcgaa aagcttgccg ttaaagtgtc tgcgtaaaaa	180
gcaaacgtag gacagcctgc aaaaatcaaa gaaatgttcc agcaaatgta tgaacgttc	240
ggcagacttg atgtttttgt caataatgcc gcttcaggag tactaagacc tgcctggaa	300
ttagaagaaa cacactggga ctggacgatg aacattaatg cgaagcatt gcttttctgc	360
gctcaggaag ctgccaagct aatggagaag aacggtggcg ggcattatgt cagcattagt	420
tcattaggct ctatccgcta tcttgaaaac tacaccacgg tcggtgtatc aaaagcagcg	480
ttagaggctt taaccggtta tcttgccgtt gagctttcac caaaacaaat tatcgtcaat	540
gctgtttcag gcggagcgat cgacacagat gcgctgaagc acttcccga tagagaagat	600
ctgcttgagg atgcgcgccca aaatacgccg gcgggacgca tggtcgaaat taaagacatg	660
gttgatactg tggagtttct agtgtcttcc aaggctgaca tgatccgcgg acagacaatt	720
atcgttgacg gcggacgctc actgctcgtt taa	753

<210> 50
 <211> 250
 <212> PRT
 <213> FabI Bacillus subtilis

<400> 50

Met Glu Gln Asn Lys Cys Ala Leu Val Thr Gly Ser Ser Arg Gly Val
 1 5 10 15

Gly Lys Ala Ala Ala Ile Arg Leu Ala Glu Asn Gly Tyr Asn Ile Val
 20 25 30

Ile Asn Tyr Ala Arg Ser Lys Lys Ala Ala Leu Glu Thr Ala Glu Glu
 35 40 45

Ile Glu Lys Leu Gly Val Lys Val Leu Val Val Lys Ala Asn Val Gly
 50 55 60

Gln Pro Ala Lys Ile Lys Glu Met Phe Gln Gln Ile Asp Glu Thr Phe
 65 70 75 80

Gly Arg Leu Asp Val Phe Val Asn Asn Ala Ala Ser Gly Val Leu Arg
 85 90 95

Pro Val Met Glu Leu Glu Glu Thr His Trp Asp Trp Thr Met Asn Ile
 100 105 110

Asn Ala Lys Ala Leu Leu Phe Cys Ala Gln Glu Ala Ala Lys Leu Met
 115 120 125

Glu Lys Asn Gly Gly Gly His Ile Val Ser Ile Ser Ser Leu Gly Ser
 130 135 140

Ile Arg Tyr Leu Glu Asn Tyr Thr Thr Val Gly Val Ser Lys Ala Ala
 145 150 155 160

Leu Glu Ala Leu Thr Arg Tyr Leu Ala Val Glu Leu Ser Pro Lys Gln
 165 170 175

Ile Ile Val Asn Ala Val Ser Gly Gly Ala Ile Asp Thr Asp Ala Leu
 180 185 190

Lys His Phe Pro Asn Arg Glu Asp Leu Leu Glu Asp Ala Arg Gln Asn
 195 200 205

Thr Pro Ala Gly Arg Met Val Glu Ile Lys Asp Met Val Asp Thr Val
 210 215 220

Glu Phe Leu Val Ser Ser Lys Ala Asp Met Ile Arg Gly Gln Thr Ile
 225 230 235 240

Ile Val Asp Gly Gly Arg Ser Leu Leu Val
 245 250

<210> 51
 <211> 780
 <212> DNA
 <213> Campylobacter jejuni NCTC 11168 FabI

<400> 51
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 aaagctatag tttatgaatt tgctaaagtg ggtgcaaata tagcttttac ttataattct 120
 aatgcgcaaa ttgctgatga aatggttcaa gatttggaga aaaattataa aatcaaaagct 180
 agagccttatg aatttaatat cttagaacct gaaacctata aagaactttt tgaaaaaatt 240
 gatgtggatt ttgatagagt ggattatttt atctcaaatg ctatcatctc aggacgtgcg 300
 gttgtagggtg gctataccaa atttatgaag ttaaaaccaa agggaattaa taacattttt 360
 acagccacag taaatgcttt tgttgtgggc gcacaagaag cagctaaaaa gatggaaaaa 420
 gtgggggggtg gaagcattat ttctatctca tctacaggaa atttagtgta tatagaaaat 480
 tattcaggtc acggtacagc aaaagccgct gtagaagcta tggcaagata tgcggctact 540
 gaacttgag aaaaaaatat ccgtgtaaat gtogtaagtg gtgggcctat taaaactgat 600
 gctttaagag cttttacaaa ttatgaagaa gtaaaacagg ctactataaa tttaaagcct 660
 taaatcgca tggggcagcc tgaagatttg gctggagcat gtctttttct ttgttcaagt 720
 aaggcaagtt ggggttacagg acatactttc atcgttgatg gtggtacaac ttttaataaa 780

<210> 52
 <211> 259
 <212> PRT
 <213> Campylobacter jejuni FabI

<400> 52

Met Asn Thr Glu Phe Gln Gly Lys Thr Leu Val Ile Ser Gly Gly Thr
 1 5 10 15

Arg Gly Ile Gly Lys Ala Ile Val Tyr Glu Phe Ala Lys Val Gly Ala
 20 25 30

Asn Ile Ala Phe Thr Tyr Asn Ser Asn Ala Gln Ile Ala Asp Glu Met
 35 40 45

Val Gln Asp Leu Glu Lys Asn Tyr Lys Ile Lys Ala Arg Ala Tyr Glu
50 55 60

Phe Asn Ile Leu Glu Pro Glu Thr Tyr Lys Glu Leu Phe Glu Lys Ile
65 70 75 80

Asp Val Asp Phe Asp Arg Val Asp Tyr Phe Ile Ser Asn Ala Ile Ile
85 90 95

Ser Gly Arg Ala Val Val Gly Gly Tyr Thr Lys Phe Met Lys Leu Lys
100 105 110

Pro Lys Gly Ile Asn Asn Ile Phe Thr Ala Thr Val Asn Ala Phe Val
115 120 125

Val Gly Ala Gln Glu Ala Ala Lys Arg Met Glu Lys Val Gly Gly Gly
130 135 140

Ser Ile Ile Ser Ile Ser Ser Thr Gly Asn Leu Val Tyr Ile Glu Asn
145 150 155 160

Tyr Ser Gly His Gly Thr Ala Lys Ala Ala Val Glu Ala Met Ala Arg
165 170 175

Tyr Ala Ala Thr Glu Leu Gly Glu Lys Asn Ile Arg Val Asn Val Val
180 185 190

Ser Gly Gly Pro Ile Lys Thr Asp Ala Leu Arg Ala Phe Thr Asn Tyr
195 200 205

Glu Glu Val Lys Gln Ala Thr Ile Asn Leu Ser Pro Leu Asn Arg Met
210 215 220

Gly Gln Pro Glu Asp Leu Ala Gly Ala Cys Leu Phe Leu Cys Ser Ser
225 230 235 240

Lys Ala Ser Trp Val Thr Gly His Thr Phe Ile Val Asp Gly Gly Thr
245 250 255

Thr Phe Lys

<210> 53

<211> 789

<212> DNA

<213> Helicobacter pylori FabI

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<400> 53
atgaatggtt ccaatcacat gaaaaataaa accctagtga tcagcggcgc gactagaggg 60
attggcaagg cgatatttgt acgcttcgct caaagcggcg tgaatatcgc ttctacttac 120
aataaaaatg ttgaagaagc caacaaaatc atagaagatg tggagcaaaa atattccatt 180
aaagccaaa g cctactctct taatgtttta gagcctgagc aatacacgga gcttttcaag 240
caaatggacg ctgattttga cagagtggat ttttttattt ctaacgctat tatttatggg 300
cgttctgtcg tggggggatt tgcaccgttt atgcgattaa aacctaaggg gttaacaac 360
atttacacag ccaccgtgtt agcgttcgtc gtaggggctc aagaagcgcg aaaacgcatg 420
caaaaaatag gcgggtggggc gatcgtgagc ttaagtctta ccgggaatct agtttatatg 480
cctaattacg ccgggcgatg caattccaaa aacgcgctag aaaccatggt caaatacgct 540
gccgtggatt taggcgaatt taacattaga gtgaatgcgg ttagtggcgg gcctattgat 600
acggacgctt tgaagaacct cctgattat gtggagatta aagaaaaagt agaagagcaa 660
tcgcccctaa aacgcatggg caatcctaac gatctagcgg gagcgggtta ttttttatgc 720
gatgagaccc aaagcgggtg gcttacaggg caaacgatcg ttgtagatgg cgggactact 780
tttaataaa 789

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<210> 54
<211> 262
<212> PRT
<213> Helicobacter pylori FabI

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<400> 54

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Met Asn Gly Ser Asn His Met Lys Asn Lys Thr Leu Val Ile Ser Gly
1          5          10          15

```

```

Ala Thr Arg Gly Ile Gly Lys Ala Ile Phe Val Arg Phe Ala Gln Ser
20          25          30

```

```

Gly Val Asn Ile Ala Phe Thr Tyr Asn Lys Asn Val Glu Glu Ala Asn
35          40          45

```

```

Lys Ile Ile Glu Asp Val Glu Gln Lys Tyr Ser Ile Lys Ala Lys Ala
50          55          60

```

```

Tyr Ser Leu Asn Val Leu Glu Pro Glu Gln Tyr Thr Glu Leu Phe Lys
65          70          75          80

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Gln Ile Asp Ala Asp Phe Asp Arg Val Asp Phe Phe Ile Ser Asn Ala
85          90          95

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Ile Ile Tyr Gly Arg Ser Val Val Gly Gly Phe Ala Pro Phe Met Arg
 100 105 110

Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val Leu Ala
 115 120 125

Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys Ile Gly
 130 135 140

Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val Tyr Met
 145 150 155 160

Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu Thr Met
 165 170 175

Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg Val Asn
 180 185 190

Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala Phe Pro
 195 200 205

Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro Leu Lys
 210 215 220

Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe Leu Cys
 225 230 235 240

Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val Val Asp
 245 250 255

Gly Gly Thr Thr Phe Lys
 260

<210> 55
 <211> 843
 <212> DNA
 <213> FabI Streptomyces collinus

<400> 55
 atgaacagcc ctcaccagca gcagaccgcc gaccgccggc aggtctccct gatcaccggg 60
 gcctcgcgcg gcatcgcccg caccctggcc ctcaccctcg ccgcgccggg tggcaccgtg 120
 gtctcaact acaagaagaa cgccgacctg gcacagaaga ccgtcgccga ggtcgaggag 180
 gccggtggcc agggcttcgc ggtccaggcg gacgtcgaga ccaccgaggg ggtcacggcg 240
 ctgttcgacg aggtggcgca gcgctcgggg aggtctcgatc attctgtctc caacgcggcg 300

ggcagcgcg tcaagaacat cgtcgatctc ggcccgcacc acctggaccg ctgcgtacgg 360
 atgaacctgc ggcctctcgt gctgggggcg caacaggccg tgaagctgat ggacaacggc 420
 ggacggatcg tcgcgctgtc ctctacggc tcggtccgcg cctaccaccac ctacgcgatg 480
 ctccggcgga tgaagcccg catcgagtca tgggtgcggt acatggcggt ggagttcgct 540
 ccttacggca tcaacgtcaa cgcggtcaac ggcggcctga tcgaactcga ttcgctggag 600
 ttcttctaca acgtcgaggg catgccgccc atgcaggggc tcctcgaccg catccccgcg 660
 cgccgtccgg gcaccgtaca ggagatggcc gacaccatcg cttctctgct cggcgacggga 720
 gcgggttaca tcaccgggca gaccctcgtg gtcgacggcg ggctcagcat cgtcgcccg 780
 ccgttcttcg cggacgcggg tgaggcgctc gagctgcgc cccggccgac gcgagacgcc 840
 tga 843

<210> 56
 <211> 280
 <212> PRT
 <213> FabI Streptomyces collinus

<400> 56

Met Asn Ser Pro His Gln Gln Gln Thr Ala Asp Arg Arg Gln Val Ser
 1 5 10 15

Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Arg Thr Leu Ala Leu Thr
 20 25 30

Leu Ala Arg Arg Gly Gly Thr Val Val Val Asn Tyr Lys Lys Asn Ala
 35 40 45

Asp Leu Ala Gln Lys Thr Val Ala Glu Val Glu Glu Ala Gly Gly Gln
 50 55 60

Gly Phe Ala Val Gln Ala Asp Val Glu Thr Thr Glu Gly Val Thr Ala
 65 70 75 80

Leu Phe Asp Glu Val Ala Gln Arg Cys Gly Arg Leu Asp His Phe Val
 85 90 95

Ser Asn Ala Ala Ala Ser Ala Phe Lys Asn Ile Val Asp Leu Gly Pro
 100 105 110

His His Leu Asp Arg Ser Tyr Ala Met Asn Leu Arg Pro Phe Val Leu
 115 120 125

Gly Ala Gln Gln Ala Val Lys Leu Met Asp Asn Gly Gly Arg Ile Val

130

135

140

Ala Leu Ser Ser Tyr Gly Ser Val Arg Ala Tyr Pro Thr Tyr Ala Met
 145 150 155 160

Leu Gly Gly Met Lys Ala Ala Ile Glu Ser Trp Val Arg Tyr Met Ala
 165 170 175

Val Glu Phe Ala Pro Tyr Gly Ile Asn Val Asn Ala Val Asn Gly Gly
 180 185 190

Leu Ile Asp Ser Asp Ser Leu Glu Phe Phe Tyr Asn Val Glu Gly Met
 195 200 205

Pro Pro Met Gln Gly Val Leu Asp Arg Ile Pro Ala Arg Arg Pro Gly
 210 215 220

Thr Val Gln Glu Met Ala Asp Thr Ile Ala Phe Leu Leu Gly Asp Gly
 225 230 235 240

Ala Gly Tyr Ile Thr Gly Gln Thr Leu Val Val Asp Gly Gly Leu Ser
 245 250 255

Ile Val Ala Pro Pro Phe Phe Ala Asp Ala Gly Glu Ala Leu Glu Leu
 260 265 270

Pro Pro Arg Pro Thr Arg Asp Ala
 275 280

<210> 57

<211> 176

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabI Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X=Ala, Gly, Ser, Pro, or Thr

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> X=Pro, Ala, Gly, Thr, or Ser

<220>

<221> MISC_FEATURE

<222> (6)..(6)
<223> X=Ile, Val, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (8)..(127)
<223> X=any amino acid and up to 20 may be absent

<220>
<221> MISC_FEATURE
<222> (130)..(130)
<223> X=Glu, Gln, Asn, or Asp

<220>
<221> MISC_FEATURE
<222> (132)..(132)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (134)..(134)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (136)..(159)
<223> X=any amino acid and up to 6 may be absent

<220>
<221> MISC_FEATURE
<222> (161)..(166)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (168)..(168)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (170)..(170)
<223> X=Val, Ile, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (172)..(172)
<223> X=Thr, Ala, Ser, Pro, or Gly

<220>
<221> MISC_FEATURE
<222> (173)..(174)

<223> X=any amino acid

<220>

<221> MISC_FEATURE

<222> (175)..(175)

<223> X=Lys, Arg, or His

<400> 57

Gly Xaa Xaa Arg Gly Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Gln Xaa Ala Xaa Lys Xaa Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Ala Xaa Glu Xaa Xaa Xaa Xaa Tyr
165 170 175

<210> 58

<211> 8

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: A FabI Consensus Sequence

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X=Ala, Gly, Ser, Pro, or Thr

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X=Pro, Ala, Gly, Thr, or Ser

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> X=Ile, Val, Leu, or Met

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> X=any amino acid

<400> 58

Gly Xaa Xaa Arg Gly Xaa Gly Xaa
 1 5

<210> 59
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 59
 tctagacata tgaaaacgcg tattacagaa tta

33

<210> 60
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 60
 ggatcctaga tactgggcac cttgacc

27

<210> 61
 <211> 5
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: A SDR Consensus Sequence

<220>
 <221> MISC_FEATURE
 <222> (2)..(4)
 <223> X=any amino acid

<400> 61

Tyr Xaa Xaa Xaa Lys
 1 5

<210> 62
 <211> 8
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: A Enoyl Reductase Consensus Sequence

<220>
 <221> MISC_FEATURE
 <222> (2)..(7)
 <223> X=any amino acid

<400> 62

Thr Xaa Xaa Xaa Xaa Xaa Lys
 1 5